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The invention relates to methods to select breeding animals or animals destined for slaughter for having desired genotypic or potential phenotypic properties, in particular related to muscle mass and/or fat deposition. Breeding schemes for domestic animals have so far focused on farm performance traits and carcass quality. This has resulted in substantial improvements in traits like reproductive success, milk production, lean/fat ratio, prolificacy, growth rate and feed efficiency. Relatively simple performance test data have been the basis for these improvements, and selected traits were assumed to be influenced by a large number of genes, each of small effect (the infinitesimal gene model). There are now some important changes occurring in this area. First, the breeding goal of some breeding organisations has begun to include meat quality attributes in addition to the "traditional" production traits. Secondly, evidence is accumulating that current and new breeding goal traits may involve relatively large effects (known as major genes), as opposed to the infinitesimal model that has been relied on so far.

Modern DNA-technologies provide the opportunity to exploit these major genes, and this approach is a very promising route for the improvement of meat quality, especially since direct meat quality assessment is not viable for potential breeding animals. Also for other traits such as lean/fat ratio, growth rate and feed efficiency, modern DNA technology can be very effective. Also these traits are not always easy to measure in the living animal.

The evidence for several of the major genes originally obtained using segregation analysis, i.e. without any DNA marker information. Afterwards molecular studies were performed to detect the location of these

genes on the genetic map. In practice, and except for alleles of very large effect, DNA studies are required to dissect the genetic nature of most traits of economic importance. DNA markers can be used to localise genes or alleles responsible for qualitative traits like coat colour, and they can also be used to detect genes or alleles with substantial effects on quantitative traits like growth rate, IMF etc. In this case the approach is referred to as QTL (quantitative trait locus) mapping, wherein a QTL comprises at least a part of the nucleic acid genome of an animal where genetic information capable of influencing said quantitative trait (in said animal or in its offspring) is located. Information at DNA level can not only help to fix a specific major gene in a population, but also assist in the selection of a quantitative trait which is already selected for. Molecular information in addition to phenotypic data can increase the accuracy of selection and therefore the selection response.

Improving meat quality or carcass quality is not just about changing levels of traits like tenderness or marbling, but it is also about increasing uniformity. The existence of major genes provides excellent opportunities for improving meat quality because it allows large steps to be made in the desired direction. Secondly, it will help to reduce variation, since we can fix relevant genes in our products. Another aspect is that selecting for major genes allows differentiation for specific markets. Studies are underway in several species, particularly, pigs, sheep, deer and beef cattle.

In particular, intense selection for meat production has resulted in animals with extreme muscularity and leanness in several livestock species. In recent years it has become feasible to map and clone several of the genes causing these phenotypes, paving the way towards more efficient marker assisted selection, targeted drug development (performance enhancing products) and transgenesis. Mutations in the ryanodine receptor (Fuji

et al, 1991; MacLennan and Phillips, 1993) and myostatin (Grobet et al, 1997; Kambadur et al, 1997; McPherron and Lee, 1997) have been shown to cause muscular hypertrophies in pigs and cattle respectively, while
5 genes with major effects on muscularity and/or fat deposition have for instance been mapped to pig chromosome 4 (Andersson et al, 1994) and sheep chromosome 18 (Cocket et al, 1996).

However, although there have been successes in
10 identifying QTLs, the information is currently of limited use within commercial breeding programmes. Many workers in this field conclude that it is necessary to identify the particular genes underlying the QTL. This is a substantial task, as the QTL region is usually relatively
15 large and may contain many genes. Identification of the relevant genes from the many that may be involved thus remains a significant hurdle in farm animals.

The invention provides a method for selecting a
20 domestic animal for having desired genotypic or potential phenotypic properties comprising testing said animal for the presence of a parentally imprinted qualitative or quantitative trait locus (QTL). Herein, a domestic animal is defined as an animal being selected or having been
25 derived from an animal having been selected for having desired genotypic or potential phenotypic properties.

Domestic animals provide a rich resource of genetic and phenotypic variation, traditionally domestication involves selecting an animal or its offspring for having
30 desired genotypic or potential phenotypic properties. This selection process has in the past century been facilitated by growing understanding and utilisation of the laws of Mendelian inheritance. One of the major problems in breeding programs of domestic animals is the
35 negative genetic correlation between reproductive capacity and production traits. This is for example the case in cattle (a high milk production generally results

in slim cows and bulls) poultry, broiler lines have a low level of egg production and layers have generally very low muscle growth), pigs (very prolific sows are in general fat and have comparatively less meat) or sheep (high prolific breeds have low carcass quality and vice versa). The invention now provides that knowledge of the parental imprinting character of various traits allows to select for example sire lines homozygous for a paternally imprinted QTL for example linked with muscle production or growth; the selection for such traits can thus be less stringent in dam lines in favour of the reproductive quality. The phenomenon of genetic or parental imprinting has never been utilised in selecting domestic animals, it was never considered feasible to employ this elusive genetic characteristic in practical breeding programmes. The invention provides a breeding programme, wherein knowledge of the parental imprinting character of a desired trait, as demonstrated herein, results in a breeding programme, for example in a BLUP programme, with a modified animal model. This increases the accuracy of the breeding value estimation and speeds up selection compared to conventional breeding programmes. Until now, the effect of a paternally imprinted trait in the estimation of a conventional BLUP programme was neglected; using and understanding the parental character of the desired trait, as provided by the invention, allows selecting on parental imprinting, even without DNA testing. For example, selecting genes characterised by paternal imprinting is provided to help increase uniformity; a (terminal) parent homozygous for the "good or wanted" alleles will pass them to all offspring, regardless of the other parent's alleles, and the offspring will all express the desired parent's alleles. This results in more uniform offspring. Alleles that are interesting or favourable from the maternal side or often the ones that have opposite effects to alleles from the paternal side. For example, in meat animals such as pigs alleles linked with meat quality traits such as intra-

muscular fat or muscle mass could be fixed in the dam lines while alleles linked with reduced back fat could be fixed in the sire lines. Other desirable combinations are for example fertility and/or milk yield in the female line with growth rates and/or muscle mass in the male lines.

In a preferred embodiment, the invention provides a method for selecting a domestic animal for having desired genotypic or potential phenotypic properties comprising testing a nucleic acid sample from said animal for the presence of a parentally imprinted quantitative trait locus (QTL). A nucleic acid sample can in general be obtained from various parts of the animal's body by methods known in the art. Traditional samples for the purpose of nucleic acid testing are blood samples or skin or mucosal surface samples, but samples from other tissues can be used as well, in particular sperm samples, oocyte or embryo samples can be used. In such a sample, the presence and/or sequence of a specific nucleic acid, be it DNA or RNA, can be determined with methods known in the art, such as hybridisation or nucleic acid amplification or sequencing techniques known in the art. The invention provides testing such a sample for the presence of nucleic acid wherein a QTL or allele associated therewith is associated with the phenomenon of parental imprinting, for example where it is determined whether a paternal or maternal allele of said QTL is capable of being predominantly expressed in said animal.

The purpose of breeding programs in livestock is to enhance the performances of animals by improving their genetic composition. In essence this improvement accrues by increasing the frequency of the most favourable alleles for the genes influencing the performance characteristics of interest. These genes are referred to as QTL. Until the beginning of the nineties, genetic improvement was achieved via the use of biometrical methods, but without molecular knowledge of the underlying QTL.

Since the beginning of the nineties and due to recent developments in genomics, it is conceivable to identify the QTL underlying a trait of interest. The invention now provides identifying and using parentally imprinted QTLs which are useful for selecting animals by mapping quantitative trait loci. Again, the phenomenon of genetic or paternal imprinting has never been utilised in selecting domestic animals, it was never considered feasible to employ this elusive genetic characteristic in practical breeding programmes. For example Kovacs and Kloting (Biochem. Mol. Biol. Int. 44:399-405, 1998), where parental imprinting is not mentioned, and not suggested, found linkage of a trait in female rats, but not in males, suggesting a possible sex specificity associated with a chromosomal region, which of course excludes parental imprinting, a phenomenon wherein the imprinted trait of one parent is preferably but gender-aspecifically expressed in his or her offspring.

The invention provides the initial localisation of a parentally imprinted QTL on the genome by linkage analysis with genetic markers, and the actual identification of the parentally imprinted gene(s) and causal mutations therein. Molecular knowledge of such a parentally imprinted QTL allows for more efficient breeding designs herewith provided. Applications of molecular knowledge of parentally imprinted QTLs in breeding programs include: marker assisted segregation analysis to identify the segregation of functionally distinct parentally imprinted QTL alleles in the populations of interest, marker assisted selection (MAS) performed within lines to enhance genetic response by increasing selection accuracy, selection intensity or by reducing the generation interval using the understanding of the phenomenon of parental imprinting, marker assisted introgression (MAI) to efficiently transfer favourable parentally imprinted QTL alleles from a donor to a recipient population, genetic engineering of the identified parentally QTL and genetic modification of the breeding stock using transgenic technology, development

of performance enhancing products using targeted drug development exploiting molecular knowledge of said QTL.

The inventors undertook two independent experiments to determine the practical use of parental imprinting of a QTL.

In a first experiment, performed in a previously described Piétrain x Large White intercross, the likelihood of the data were computed under a model of paternal (paternal allele only expressed) and maternal imprinting (maternal allele only expressed) and compared with the likelihood of the data under a model of a conventional "Mendelian" QTL. The results strikingly demonstrated that the QTL was indeed paternally expressed, the QTL allele (Piétrain or Large White) inherited from the F₁ sow having no effect whatsoever on the carcass quality and quantity of the F₂ offspring. It was seen that very significant lodscores were obtained when testing for the presence of a paternally expressed QTL, while there was no evidence at all for the segregation of a QTL when studying the chromosomes transmitted by the sows. The same tendency was observed for all traits showing that the same imprinted gene is responsible for the effects observed on the different traits. Table 1 reports the maximum likelihood (ML) phenotypic means for the F₂ offspring sorted by inherited paternal QTL allele.

In a second experiment performed in the Wild Boar X Large White intercross, QTL analyses of body composition, fatness, meat quality, and growth traits was carried out with the chromosome 2 map using a statistical model testing for the presence of an imprinting effect. Clear evidence for a paternally expressed QTL located at the very distal tip of 2p was obtained (Fig. 2; Table1). The clear paternal expression of a QTL is illustrated by the least squares means which fall into two classes following the population origin of the paternally inherited allele (Table 1). For a given paternally imprinted QTL, implementation of marker assisted segregation analysis, selection (MAS) and introgression (MAI), can be performed

using genetic markers that are linked to the QTL, genetic markers that are in linkage disequilibrium with the QTL, or using the actual causal mutations within the QTL.

Understanding the parent-of-origin effect

5 characterising a QTL allows for its optimal use in breeding programs. Indeed, marker assisted segregation analysis under a model of parental imprinting will yield better estimates of QTL allele effects. Moreover it allows for the application of specific breeding schemes
10 to optimally exploit a QTL. In one embodiment of the invention, the most favourable QTL alleles would be fixed in breeding animal lines and for example used to generate commercial, crossbred males by marker assisted selection (MAS, within lines) and marker assisted introgression
15 (MAI, between lines). In another embodiment, the worst QTL alleles would be fixed in the animal lines used to generate commercial crossbred females by MAS (within lines) and MAI (between lines).

In a preferred embodiment of the invention, said
20 animal is a pig. Note for example that the invention provides the insight that today half of the offspring from commercially popular Piétrain, Large White crossbred boars inherit an unfavourable Large White muscle mass QTL as provided by the invention causing considerable loss,
25 and the invention now for example provides the possibility to select the better half of the population in that respect. However, it is also possible to select commercial sow lines enriched with the in the boars unfavourable alleles, allowing to equip the sows with
30 other alleles more desirable for for example reproductive purposes.

In a preferred embodiment of a method provided by the invention, said QTL is located at a position corresponding to a QTL located at chromosome 2 in the
35 pig. For example, it is known from comparative mapping data between pig and human, including bidirectional chromosome painting, that SSC2p is homologous to HSA11pter-q13^{11,12}. HSA11pter-q13 is known to harbour a

cluster of imprinted genes: IGF2, INS2, H19, MAH2, P57^{KIP2}, K_LQTL1, Tapal./CD81, Orct12, Impt1 and Ip1. The cluster of imprinted genes located in HSA11pter-q13 is characterised by 8 maternally expressed genes H19, MASH2, P57^{KIP2}, K_LQTL1, TAPAL/CD81, ORCTL2, IMPT1 and IP1, and two paternally expressed genes: IGF2 and INS. However, Johanson et al (Genomics 25:682-690, 1995) and Reik et al (Trends in Genetics, 13:330-334, 1997) show that the whereabouts of these loci in various animals are not clear. For example, the HSA11 and MMU7 loci do not correspond among each other, the MMU7 and the SSC2 loci do not correspond, whereas the HSA11 and SSC2 loci seem to correspond, and no guidance is given where one or more of for example the above identified parentally expressed individual genes are localised on the three species' chromosomes.

Other domestic animals, such as cattle, sheep, poultry and fish, having similar regions in their genome harbouring such a cluster of imprinted genes or QTLs, the invention herewith provides use of these orthologous regions of other domestic animals in applying the phenomenon of parental imprinting in breeding programmes. In pigs, said cluster is mapped at around position 2p1.7 of chromosome 2, however, a method as provided by the invention employing (fragments of) said maternally or paternally expressed orthologous or homologous genes or QTLs are advantageously used in other animals as well for breeding and selecting purposes. For example, a method is provided wherein said QTL is related to the potential muscle mass and/or fat deposition, preferably with limited effects on other traits such as meat quality and daily gain of said animal or wherein said QTL comprises at least a part of an insulin-like growth factor-2 (IGF2) allele. Reik et al (Trends in Genetics, 13:330-334, 1997) explain that this gene in humans is related to Beckwith-Wiedemann syndrome, an apparently parentally imprinted disease syndrome most commonly seen with human foetuses, where the gene has an important role in prenatal

development. No relationship is shown or suggested with postnatal development relating to muscle development or fatness in (domestic) animals.

In a preferred embodiment, the invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7. In particular, the invention relates to the use of genetic markers for the telomeric end of pig chromosome 2p in marker selection (MAS) of a parentally imprinted Quantitative Trait Locus (QTL) affecting carcass yield and quality in pigs. Furthermore, the invention relates to the use of genetic markers associated with the IGF2 locus in MAS in pigs, such as polymorphisms and microsatellites and other characterising nucleic acid sequences shown herein, such as shown in figures 4 to 10. In a preferred embodiment, the invention provides a QTL located at the distal tip of *Sus scrofa* chromosomes 2 with effects on various measurements of carcass quality and quantity, particularly muscle mass and fat deposition.

In a first experiment, a QTL mapping analysis was performed in a Wild Boar X Large White intercross counting 200 F₂ individuals. The F₂ animals were sacrificed at a live weight of at least 80 kg or at a maximum age of 190 days. Phenotypic data on birth weight, growth, fat deposition, body composition, weight of internal organs, and meat quality were collected; a detailed description of the phenotypic traits are provided by Andersson et al¹ and Andersson-Eklund et al⁴.

A QTL (without any significant effect on back-fat thickness) at an unspecified locus on the proximal end of chromosome 2 with moderate effect on muscle mass, and located about 30cM away from the parentally imprinted QTL reported here, was previously reported by the inventors; whereas the QTL as now provided has a very large effect, explaining at least 20-30% of variance, making the QTL of

the present invention commercially very attractive, which is even more so because the present QTL is parentally imprinted. The marker map of chromosome 2p was improved as part of this invention by adding microsatellite markers in order to cover the entire chromosome arm. The following microsatellite markers were used: *Swc9*, *Sw2443*, *Sw2623*, and *Swr2516*, all from the distal end of 2p¹. QTL analyses of body composition, fatness, meat quality, and growth traits were carried out with the new chromosome 2 map. Clear evidence for a QTL located at the very distal tip of 2p was obtained (Fig. 1; Table 1). The QTL had very large effects on lean meat content in ham and explained an astonishing 30% of the residual phenotypic variance in the F₂ population. Large effects on the area of the longissimus dorsi muscle, on the weight of the heart, and on back-fat thickness (subcutaneous fat) were also noted. A moderate effect on one meat quality trait, reflectance value, was indicated. The QTL had no significant effect on abdominal fat, birth weight, growth, weight of liver, kidney, or spleen (data not shown). The Large White allele at this QTL was associated with larger muscle mass and reduced back-fat thickness consistent with the difference between this breed and the Wild Boar population.

In a second experiment, QTL mapping was performed in a Piétrain X Large White intercross comprising 1125 F₂ offspring. The Large White and Piétrain parental breeds differ for a number of economically important phenotypes. Piétrains are famous for their exceptional muscularity and leanness¹⁰ (Figure 2, while Large Whites show superior growth performance. Twenty-one distinct phenotypes measuring growth performance (5), muscularity (6), fat deposition (6), and meat quality (4), were recorded on all F₂ offspring. In order to map QTL underlying the genetic differences between these breeds, the inventors undertook a whole genome scan using microsatellite markers on an initial sample of 677 F₂ individuals. The following microsatellite marker map was used to analyse

- chromosome 2; SW2443, SWC9 and SW2623, SWR2516-(0,20)-SWR783-(0,29)-SW240-(0,20)-SW776-(0,08)-S0010-(0,04)-SW1695-(0,36)-SWR308. Analysis of pig chromosome 2 using a Maximum Likelihood multipoint algorithm, revealed
- 5 highly significant lodscores (up to 20) for three of the six phenotypes measuring muscularity (% lean cuts, % ham, % loin) and three of the six phenotypes measuring fat deposition (back-fat thickness (BFT), % backfat, % fat cuts) at the distal end of the short arm of chromosome 2
- 10 (Figure 1). Positive lodscores were obtained in the corresponding chromosome region for the remaining six muscularity and fatness phenotypes, however, not reaching the experiment-wise significance threshold ($\alpha=5\%$). There was no evidence for an effect of the corresponding QTL on
- 15 growth performance (including birth weight) or recorded meat quality measurements (data not shown). To confirm this finding, the remaining sample of 355 F₂ offspring was genotyped for the four most distal 2p markers and QTL analysis performed for the traits yielding the highest
- 20 lodscores in the first analysis. Lodscores ranged from 2.1 to 7.7, clearly confirming the presence of a major QTL in this region. Table 2 reports the corresponding ML estimates for the three genotypic means as well as the residual variance. Evidence based on marker assisted
- 25 segregation analysis points towards residual segregation at this locus within the Piétrain population.
- These experiments therefore clearly indicated the existence of a QTL with major effect on carcass quality and quantity on the telomeric end of pig
- 30 chromosome arm 2p; the likely existence of an allelic series at this QTL with at least three alleles: Wild-Boar < Large White < Piétrain, and possibly more given the observed segregation within the Piétrain breed.
- The effects of the identified QTL on muscle mass and
- 35 fat deposition are truly major, being of the same magnitude of those reported for the *CRC* locus though apparently without the associated deleterious effects on meat quality. We estimate that both loci jointly explain

close to 50% of the Piétrain versus Large White breed difference for muscularity and leanness. The QTL had very large effects on lean meat content in ham and explained an astonishing 30% of the residual phenotypic variance in the F_2 population. Large effects on the area of the longissimus dorsi muscle, on the weight of the heart, and on back-fat thickness (subcutaneous fat) were also noted. A moderate effect on one meat quality trait, reflectance value, was indicated. The QTL had no significant effect on abdominal fat, birth weight, growth, weight of liver, kidney, or spleen (data not shown). The Large White allele at this QTL, when compared to the Wild Boar allele, was associated with larger muscle mass and reduced back-fat thickness consistent with the difference between this breed and the Wild Boar population. The strong imprinting effect observed for all affected traits shows that a single causative locus is involved. The pleiotropic effects on skeletal muscle mass and the size of the heart appear adaptive from a physiological point of view as a larger muscle mass requires a larger cardiac output.

In a further embodiment, the invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7., wherein said QTL comprises at least a part of a *Sus scrofa* insulin-like growth factor-2 (IGF2) allele or a genomic area closely related thereto, such as polymorphisms and microsatellites and other characterising nucleic acid sequences shown herein, such as shown in figures 4 to 10. The important role of IGF2 for prenatal development is well-documented from knock-out mice as well as from its causative role in the human Beckwith-Wiedemann syndrome. This invention demonstrates an important role for the IGF2-region also for postnatal development.

To show the role of *Igf2* the inventors performed the following three experiments:

A genomic *IGF2* clone was isolated by screening a porcine BAC library. FISH analysis with this BAC clone
5 gave a strong consistent signal on the terminal part of chromosome 2p.

A polymorphic microsatellite is located in the 3'UTR of *IGF2* in mice (GenBank U71085), humans (GenBank S62623), and horse (GenBank AF020598). The possible
10 presence of a corresponding porcine microsatellite was investigated by direct sequencing of the *IGF2* 3'UTR using the BAC clone. A complex microsatellite was identified about 800bp downstream of the stop codon; a sequence comparison revealed that this microsatellite was
15 identical to a previously described anonymous microsatellite, *Swc9*⁶. This marker was used in the initial QTL mapping experiments and its location on the genetic map correspond with the most likely position of the QTL both in the Piétrain X Large White and in the Large White
20 x Wild Boar pedigree.

Analysis of skeletal muscle and liver cDNA from 10-week old fetuses heterozygous for a nt241 (G-A) transversion in the second exon of the porcine *IGFII* gene and *SWC9*, shows that the *IGFII* gene is imprinted in these
25 tissues in the pig as well and only expressed from the paternal allele.

Based on a published porcine adult liver cDNA sequence¹⁶, the inventors designed primer pairs allowing to amplify the entire *IgfII* coding sequence with 222 bp
30 of leader and 280 bp of trailer sequence from adult skeletal muscle cDNA. Piétrain and Large White RT-PCR products were sequenced indicating that the coding sequences are identical in both breeds and with the published sequence. However, a G→A transition was found
35 in the leader sequence corresponding to exon 2 in man. Following conventional nomenclature, this polymorphism will be referred to as nt241(G-A). We developed a screening test for this single nucleotide polymorphism

9(SNP) based on the ligation amplification reaction (LAR), allowing us to genotype our pedigree material. Based on these data, *IgfII* was shown to colocalize with the SWC9 microsatellite marker ($\theta=0\%$), therefore

5 virtually coinciding with the most likely position of the QTL, and well within the 95% support interval for the QTL. Subsequent sequence analysis demonstrated that the microsatellite marker SWC9 is actually located within the 3'UTR of the *IgfII* gene.

10 As previously mentioned, the knowledge of this QTL provides a method for the selection of animals such as pigs with improved carcass merit. Different embodiments of the invention are envisaged, including: marker assisted segregation analysis to identify the
15 segregation of functionally distinct QTL alleles in the populations of interest; marker assisted selection (MAS) performed within lines to enhance genetic response by increasing selection accuracy, selection intensity or by reducing the generation interval; marker assisted
20 introgression (MAI) to efficiently transfer favourable QTL alleles from a donor to a recipient population, thereby enhancing genetic response in the recipient population. Implementation of embodiments marker assisted segregation analysis, selection (MAS) and introgression
25 (MAI), can be performed using genetic markers that are linked to the QTL; genetic markers that are in linkage disequilibrium with the QTL, the actual causal mutations within the QTL.

In a further embodiment, the invention provides a
30 method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7., wherein said QTL is
35 paternally expressed, i.e. is expressed from the paternal allele. In man and mouse, *Igf2* is known to be imprinted and to be expressed exclusively from the paternal allele in several tissues. Analysis of skeletal muscle cDNA from

pigs heterozygous for the SNP and/or SWC9, shows that the same imprinting holds in the pig as well. Understanding the parent-of-origin effect characterising the QTL as provided by the invention now allows for its optimal use in breeding programs. Indeed, today half of the offspring from commercially popular Piétrain x Large White crossbred boars inherit the unfavourable Large White allele causing considerable loss. Using a method as provide by the invention avoids this problem.

10 The invention furthermore provides an isolated and/or recombinant nucleic acid or functional fragment derived thereof comprising a parentally imprinted quantitative trait locus (QTL) or fragment thereof capable of being predominantly expressed by one parental
15 allele. Having such a nucleic acid as provided by the invention available allows constructing transgenic animals wherein favourable genes are capable of being exclusively or predominantly expressed by one parental allele, thereby equipping the offspring of said animal
20 homozygous for a desired trait with desired properties related to that parental allele that is expressed.

In a preferred embodiment, the invention provides an isolated and/or recombinant nucleic acid or fragment derived thereof comprising a synthetic parentally
25 imprinted quantitative trait locus (QTL) or functional fragment thereof derived from at least one chromosome. Synthetic herein describes a parentally expressed QTL wherein various elements are combined that originate from distinct locations from the genome of one or more
30 animals. The invention provides recombinant nucleic acid wherein sequences related to parental imprinting of one QTL are combined with sequences relating to genes or favourable alleles of a second QTL. Such a gene construct is favourably used to obtain transgenic animals wherein
35 the second QTL has been equipped with paternal imprinting, as opposed to the inheritance pattern in the native animal from which the second QTL is derived. Such a second QTL can for example be derived from the same

chromosome where the parental imprinting region is located, but can also be derived from a different chromosome from the same or even a different species. In the pig, such a second QTL can for example be related to an oestrogen receptor (ESR)-gene (Rothschild et al, PNAS, 93, 201-201, 1996) or a FAT-QTL (Andersson, Science, 263, 1771-1774, 1994) for example derived from an other pig chromosome, such as chromosome 4. A second or further QTL can also be derived from another (domestic) animal or a human.

The invention furthermore provides an isolated and/or recombinant nucleic acid or functional fragment derived thereof at least partly corresponding to a QTL of a pig located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7 wherein said QTL is related to the potential muscle mass and/or fat deposition of said pig and/or wherein said QTL comprises at least a part of a *Sus scrofa* insulin-like growth factor-2 (IGF2) allele, preferably at least spanning a region between INS and H19, or preferably derived from a domestic pig, such as a Pietrain, Meishan, Duroc, Landrace or Large White, or from a Wild Boar. For example, a genomic IGF2 clone was isolated by screening a porcine BAC library. FISH analysis with this BAC clone gave a strong consistent signal on the terminal part of chromosome 2p. A polymorphic microsatellite is located in the 3'UTR of IGF2 in mice (GenBank U71085), humans (GenBank S62623), and horse (GenBank AF020598). The possible presence of a corresponding porcine microsatellite was investigated by direct sequencing of the IGF2 3'UTR using the BAC clone. A complex microsatellite was identified about 800 bp downstream of the stop codon; a sequence comparison revealed that this microsatellite is identical to a previously described anonymous microsatellite, Swc9. PCR primers were designed and the microsatellite (IGF2ms) was found to be highly polymorphic with three different alleles among the two Wild Boar founders and another two

among the eight Large White founders. *IGF2ms* was fully informative in the intercross as the breed of origin as well as the parent of origin could be determined with confidence for each allele in each F_2 animal.

5 A linkage analysis using the intercross pedigree was carried out with *IGF2ms* and the microsatellites *Sw2443*, *Sw2623*, and *Swr2516*, all from the distal end of 2p⁷. *IGF2* was firmly assigned to 2p by highly significant lod scores (e.g. $Z=89.0$, $\theta=0.003$ against *Swr2516*). Multipoint
10 analyses, including previously typed chromosome 2 markers, revealed the following order of loci (sex-average map distances in Kosambi cM): *Sw2443/Swr2516*-0.3-*IGF2*-14.9-*Sw2623*-10.3-*Sw256*. No recombinant was observed between *Sw2443* and *Swr2516*, and the suggested proximal
15 location of *IGF2* in relation to these loci is based on a single recombinant giving a lod score support of 0.8 for the reported order. The most distal marker in our previous QTL study, *Sw256*, is located about 25 cM from the distal end of the linkage group.

20 The invention furthermore provides use of a nucleic acid or functional fragment derived thereof according to the invention in a method according to the invention. In a preferred embodiment, use of a method according to invention is provided to select a breeding animal or
25 animal destined for slaughter, or embryos or semen derived from these animals for having desired genotypic or potential phenotypic properties. In particular, the invention provides such use wherein said properties are related to muscle mass and/or fat deposition. The QTL as
30 provided by the invention may be exploited or used to improve for example lean meat content or back-fat thickness by marker assisted selection within populations or by marker assisted introgression of favorable alleles from one population to another. Examples of marker
35 assisted selection using the QTL as provided by the invention are use of marker assisted segregation analysis

with linked markers or with markers in disequilibrium to identify functionally distinct QTL alleles. Furthermore, identification of a causative mutation in the QTL is now possible, again leading to identify functionally distinct QTL alleles. Such functionally distinct QTL alleles located at the distal tip of chromosome 2p with large effects on skeletal muscle mass, the size of the heart, and on back-fat thickness are also provided by the invention. The observation of a similar QTL effect in a Large White x Wild Boar as well as in a Piétrain x Large White intercross provides proof of the existence of a series of at least three distinct functional alleles. Moreover, preliminary evidence based on marker assisted segregation analysis points towards residual segregation at this locus within the Piétrain population (data not shown). The occurrence of an allelic series as provided by the invention allows identifying causal polymorphisms which - based on the quantitative nature of the observed effect - are unlikely to be gross gene alterations but rather subtle regulatory mutations. The effects on muscle mass of the three alleles rank in the same order as the breeds in which they are found i.e. Piétrain pigs are more muscular than Large White pigs that in turn have higher lean meat content than Wild Boars. The invention furthermore provides use of the alleles as provided by the invention for within line selection or for marker assisted introgression using linked markers, markers in disequilibrium or alleles comprising causative mutations.

The invention furthermore provides an animal selected by using a method according to the invention. For example, a pig characterised in being homozygous for an allele in a QTL located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7 can now be selected and is thus provided by the invention. Since said QTL is related to the potential muscle mass and/or fat deposition of said pig and/or said QTL comprises at least a part of a *Sus scrofa* insulin-like growth factor-2 (IGF2) allele, it is

possible to select promising pigs to be used for breeding or to be slaughtered. In particular an animal according to the invention which is a male is provided. Such a male, or its sperm or an embryo derived thereof can advantageously be used in breeding animals for creating breeding lines or for finally breeding animals destined for slaughter. In a preferred embodiment of such use as provided by the invention, a male, or its sperm, deliberately selected for being homozygous for an allele causing the extreme muscular hypertrophy and leanness, is used to produce offspring heterozygous for such an allele. Due to said allele's paternal expression, said offspring will also show the favourable traits for example related to muscle mass, even if the parent female has a different genetic background. Moreover, it is now possible to positively select the female(s) for having different traits, for example related to fertility, without having a negative effect on the muscle mass trait that is inherited from the allele from the selected male. For example, earlier such males could occasionally be seen with Piétrain pigs but genetically it was not understood how to most profitably use these traits in breeding programmes.

Furthermore, the invention provides a transgenic animal, sperm and an embryo derived thereof, comprising a synthetic parentally imprinted QTL or functional fragment thereof as provided by the invention, i.e. it is provided by the invention to introduce a favourable recombinant allele; for example introduce the oestrogen receptor locus related to increased litter size of an animal homozygously in a parentally imprinted region of a grandparent animal (for example the father of a hybrid sow if the region was paternally imprinted and the grandparent was a boar); to introduce a favourable fat-related allele or muscle mass-related recombinant allele in a paternally imprinted region, and so on. Recombinant alleles that are interesting or favourable from the maternal side or often the ones that have opposite effects to alleles from the paternal side. For example,

in meat animals such as pigs recombinant alleles linked with meat quality traits such as intra-muscular fat or muscle mass could be fixed in the dam lines while recombinant alleles linked with reduced back fat could be fixed in the sire lines. Other desirable combinations are for example fertility and/or milk yield in the female line with growth rates and/or muscle mass in the male lines.

The invention is further explained in the detailed description without limiting the invention.

Detailed description.

Example 1: Wild Boar x Large White intercrosses

Methods

Isolation of an *IGF2* BAC clone and fluorescent *in situ* hybridization (FISH). *IGF2* primers (F:5'-GGCAAGTTCTTCCGCTAATGA-3' and R:5'-GCACCGCAGAATTACGACAA-3') for PCR amplification of a part of the last exon and 3'UTR were designed on the basis of a porcine *IGF2* cDNA sequence (GenBank X56094). The primers were used to screen a porcine BAC library and the clone 253G10 was isolated. Crude BAC DNA was prepared as described²⁴. The BAC DNA was linearized with *EcoRV* and purified with QIAEXII (QIAGEN GmbH, Germany). The clone was labeled with biotin-14-dATP using the GIBCO-BRL Bionick labeling system (BRL18246-015). Porcine metaphase chromosomes were obtained from pokeweed (Seromed) stimulated lymphocytes using standard techniques. The slides were aged for two days at room temperature and then kept at -20°C until use. FISH analysis was carried out as previously described²⁵. The final concentration of the probe in the hybridization mix was 10 ng/μl. Repetitive sequences were suppressed with standard concentrations of porcine

genomic DNA. After post-hybridization washing, the biotinylated probe was detected with two layers of avidin-FITC (Vector A-2011). The chromosomes were counterstained with 0.3 mg/ml DAPI (4,6-Diamino-2-phenylindole; Sigma D9542), which produced a G-banding like pattern. No posthybridization banding was needed, since chromosome 2 is easily recognized without banding. A total of 20 metaphase spreads were examined under an Olympus BX-60 fluorescence microscope connected to an IMAC-CCD S30 video camera and equipped with an ISIS 1.65 (Metasystems) software.

Sequence, microsatellite, and linkage analysis.

About two µg of linearized and purified BAC DNA was used for direct sequencing with 20 pmoles of primers and BigDye Terminator chemistry (Perkin Elmer, USA). DNA sequencing was done from the 3' end of the last exon towards the 3' end of the UTR until a microsatellite was detected. A primer set (F:5'-GTTTCTCCTGTACCCACACGCATCCC-3' and R:5'-Fluorescein-CTACAAGCTGGGCTCAGGG-3') was designed for the amplification of the IGF2 microsatellite which is about 250 bp long and located approximately 800 bp downstream from the stop codon. The microsatellite was PCR amplified using fluorescently labeled primers and the genotyping was carried out using an ABI377 sequencer and the GeneScan/Genotyper softwares (Perkin Elmer, USA). Two-point and multipoint linkage analysis were done with the Cri-Map software²⁶.

Animals and phenotypic data.

The intercross pedigree comprised two European Wild Boar males and eight Large White females, 4 F₁ males and 22 F₁ females, and 200 F₂ progeny¹. The F₂ animals were sacrificed at a live weight of at least 80 kg or at a

maximum age of 190 days. Phenotypic data on birth weight, growth, fat deposition, body composition, weight of internal organs, and meat quality were collected; a detailed description of the phenotypic traits are provided by Andersson et al.¹ and Andersson-Eklund et al.⁴

Statistical analysis.

Interval mapping for the presence of QTL were carried out with a least squares method developed for the analysis of crosses between outbred lines²⁷. The method is based on the assumption that the two divergent lines are fixed for alternative QTL alleles. There are four possible genotypes in the F₂ generation as regards the grandparental origin of the alleles at each locus. This makes it possible to fit three effects: additive, dominance, and imprinting². The latter is estimated as the difference between the two types of heterozygotes, the one receiving the Wild Boar allele through an F₁ sire and the one receiving it from an F₁ dam. An F-ratio was calculated using this model (with 3 d.f.) versus a reduced model without a QTL effect for each cM of chromosome 2. The most likely position of a QTL was obtained as the location giving the highest F-ratio. Genome-wise significance thresholds were obtained empirically by a permutation test²⁸ as described². The QTL model including an imprinting effect was compared with a model without imprinting (with 1 d.f.) to test whether the imprinting effect was significant.

The statistical models also included the fixed effects and covariates that were relevant for the respective traits; see Andersson-Eklund et al.⁴ for a more detailed description of the statistical models used. Family was included to account for background genetic

effects and maternal effects. Carcass weight was included as a covariate to discern QTL effects on correlated traits, which means that all results concerning body composition were compared at equal weights. Least-squares means for each genotype class at the *IGF2* locus were estimated with a single point analysis using Procedure GLM of SAS²⁹; the model included the same fixed effects and covariates as used in the interval mapping analyses. The QTL shows a clear parent of origin-specific expression and the map position coincides with that of the insulin-like growth factor II gene (*IGF2*), indicating *IGF2* as the causative gene. A highly significant segregation distortion (excess of Wild Boar-derived alleles) was also observed at this locus. The results demonstrate an important effect of the *IGF2* region on postnatal development and it is possible that the presence of a paternally expressed *IGF2*-linked QTL in humans and in rodent model organisms has so far been overlooked due to experimental design or statistical treatment of data. The study has also important implications for quantitative genetics theory and practical pig breeding.

IGF2 was identified as a positional candidate gene for this QTL due to the observed similarity between pig chromosome 2p and human chromosome 11p. A genomic *IGF2* clone was isolated by screening a porcine BAC library. FISH analysis with this BAC clone gave a strong consistent signal on the terminal part of chromosome 2p (Fig. 1). A polymorphic microsatellite is located in the 3'UTR of *IGF2* in mice (GenBank U71085), humans (GenBank S62623), and horse (GenBank AF020598). The possible presence of a corresponding porcine microsatellite was investigated by direct sequencing of the *IGF2* 3'UTR using the BAC clone. A complex microsatellite was identified about 800 bp downstream of the stop codon; a sequence comparison revealed that this microsatellite is identical

- to a previously described anonymous microsatellite, Swc9⁶. PCR primers were designed and the microsatellite (*IGF2ms*) was found to be highly polymorphic with three different alleles among the two Wild Boar founders and another two among the eight Large White founders. *IGF2ms* was fully informative in the intercross as the breed of origin as well as the parent of origin could be determined with confidence for each allele in each F₂ animal.
- 10 A linkage analysis using the intercross pedigree was carried out with *IGF2ms* and the microsatellites Sw2443, Sw2623, and Swr2516, all from the distal end of 2p⁷. *IGF2* was firmly assigned to 2p by highly significant lod scores (e.g. Z=89.0, $\theta=0.003$ against Swr2516). Multipoint
- 15 analyses, including previously typed chromosome 2 markers⁸, revealed the following order of loci (sex-average map distances in Kosambi cM): Sw2443/Swr2516-0.3-*IGF2*-14.9-Sw2623-10.3-Sw256. No recombinant was observed between Sw2443 and Swr2516, and the suggested proximal
- 20 location of *IGF2* in relation to these loci is based on a single recombinant giving a lod score support of 0.8 for the reported order. The most distal marker in our previous QTL study, Sw256, is located about 25 cM from the distal end of the linkage group.
- 25 QTL analyses of body composition, fatness, meat quality, and growth traits were carried out with the new chromosome 2 map using a statistical model testing for the possible presence of an imprinting effect as expected for *IGF2*. Clear evidence for a paternally expressed QTL
- 30 located at the very distal tip of 2p was obtained (Fig. 2; Table 1). The QTL had very large effects on lean meat content in ham and explained an astonishing 30% of the residual phenotypic variance in the F₂ population. Large effects on the area of the longissimus dorsi muscle, on
- 35 the weight of the heart, and on back-fat thickness

(subcutaneous fat) were also noted. A moderate effect on one meat quality trait, reflectance value, was indicated. The QTL had no significant effect on abdominal fat, birth weight, growth, weight of liver, kidney, or spleen (data not shown). The Large White allele at this QTL was associated with larger muscle mass and reduced back-fat thickness consistent with the difference between this breed and the Wild Boar population. The strong imprinting effect observed for all affected traits strongly suggests a single causative locus. The pleiotropic effects on skeletal muscle mass and the size of the heart appear adaptive from a physiological point of view as a larger muscle mass requires a larger cardiac output. The clear paternal expression of this QTL is illustrated by the least squares means which fall into two classes following the population origin of the paternally inherited allele (Table 1). It is worth noticing though that there was a non-significant trend towards less extreme values for the two heterozygous classes, in particular for the estimated effect on the area of longissimus dorsi. This may be due to chance, but could have a biological explanation, e.g. that there is some expression of the maternally inherited allele or that there is a linked, non-imprinted QTL with minor effects on the traits in question.

The *IGF2*-linked QTL and the *FAT1* QTL on chromosome 4, 9 are by far the two loci with the largest effect on body composition and fatness segregating in this Wild Boar intercross. The *IGF2* QTL controls primarily muscle mass whereas *FAT1* has major effects on fat deposition including abdominal fat, a trait that was not affected by the *IGF2* QTL (Fig. 2). No significant interaction between the two loci was indicated and they control a very large proportion of the residual phenotypic variance in the F_2 generation. A model including both QTLs explains 33.1% of the variance for percentage lean meat in ham, 31.3% for the percentage of lean meat plus bone in back, and 26.2%

for average back fat depth (compare with a model including only chromosome 2 effects, Table 1). The two QTLs must have played a major role in the response during selection for lean growth and muscle mass in the Large White domestic pig.

A highly significant segregation distortion was observed in the *IGF2* region (excess of Wild Boar-derived alleles) as shown in Table 1 ($\chi^2=11.7$, d.f.=2; $P=0.003$). The frequency of Wild Boar-derived *IGF2* alleles was 59% in contrast to the expected 50% and there was twice as many "Wild Boar" as "Large White" homozygotes. This deviation was observed with all three loci at the distal tip and is thus not due to typing errors. The effect was also observed with other loci but the degree of distortion decreased as a function of the distance to the distal tip of the chromosome. Blood samples for DNA preparation were collected at 12 weeks of age and we are convinced that the deviation from expected Mendelian ratios was present at birth as the number of animals lost prior to blood sampling was not sufficient to cause a deviation of this magnitude. No other of the more than 250 loci analyzed in this pedigree show such a marked segregation distortion (L. Andersson, unpublished). The segregation distortion did not show an imprinting effect, as the frequencies of the two reciprocal types of heterozygotes were identical (Table 1). This does not exclude the possibility that the QTL effects and the segregation distortion are controlled by the same locus. The segregation distortion maybe due to meiotic drive favoring the paternally expressed allele during gametogenesis, as the F_1 parents were all sired by Wild Boar males. Another possibility is that the segregation distortion may be due to codominant expression of the maternal and paternal allele in some tissues and/or during a critical period of embryo development. Biallelic *IGF2* expression has been reported to occur to some extent

during human development^{10, 11} and interestingly a strong influence of the parental species background on *IGF2* expression was recently found in a cross between *Mus musculus* and *Mus spretus*¹². It is also interesting that a VNTR polymorphism at the insulin gene, which is very closely linked to *IGF2*, is associated with size at birth in humans¹³. It is possible that the *IGF2*-linked QTL in pigs has a minor effect on birth weight but in our data it was far from significant (Fig. 2) and there was no indication of an imprinting effect.

This study is an advance in the general knowledge concerning the biological importance of the *IGF2* locus. The important role of *IGF2* for prenatal development is well-documented from knock-out mice¹⁴ as well as from its causative role in the human Beckwith-Wiedemann syndrome¹⁵. This study demonstrates an important role for the *IGF2*-region also for postnatal development. It should be stressed that our intercross between outbred populations is particularly powerful to detect QTL with a parent of origin-specific effect on a multifactorial trait. This is because multiple alleles (or haplotypes) are segregating and we could deduce whether a heterozygous F_2 animal received the Wild Boar allele from the F_1 male or female. It is quite possible that the segregation of a paternally expressed *IGF2*-linked QTL affecting a trait like obesity has been overlooked in human studies or in intercrosses between inbred rodent populations because of experimental design or statistical treatment of data. An imprinting effect cannot be detected in an intercross between two inbred lines as only two alleles are segregating at each locus. Our result has therefore significant bearings on the future analysis of the association between genetic polymorphism in the *insulin-IGF2* region and Type I diabetes¹⁶, obesity¹⁷, and variation in birth weight¹³ in humans, as

well as for the genetic dissection of complex traits using inbred rodent models. A major impetus for generating an intercross between the domestic pig and its wild ancestor was to explore the possibilities to map and identify major loci that have responded to selection. We have now showed that two single QTLs on chromosome 2 (this study) and 4¹, 2 explain as much as one third of the phenotypic variance for lean meat content in the F₂ generation. This is a gross deviation from the underlying assumption in the classical infinitesimal model in quantitative genetics theory namely that quantitative traits are controlled by an infinite number of loci each with an infinitesimal effect. If a large proportion of the genetic difference between two divergent populations (e.g. Wild Boar and Large White) is controlled by a few loci, one would assume that selection would quickly fix QTL alleles with large effects leading to a selection plateau. However, this is not the experience in animal breeding programs or selection experiments where good persistent long-term selection responses are generally obtained, provided that the effective population size is reasonably large¹⁸. A possible explanation for this paradox is that QTL alleles controlling a large proportion of genetic differences between two populations may be due to several consecutive mutations; this may be mutations in the same gene or at several closely linked genes affecting the same trait. It has been argued that new mutations contribute substantially to long-term selection responses¹⁹, but the genomic distribution of such mutations are unknown.

The search for a single causative mutation is the paradigm as regards the analysis of genetic defects in mice and monogenic disorders in humans. We propose that this may not be the case for loci that have been under selection for a large number of generations in domestic animals, crops, or natural populations. This hypothesis

predicts the presence of multiple alleles at major QTL. It gains some support from our recent characterization of porcine coat color variation. We have found that both the alleles for dominant white color and for black-spotting
5 differ from the corresponding wild-type alleles by at least two consecutive mutations with phenotypic effects at the *KIT* and *MC1R* loci, respectively^{20, 21}. In this context it is highly interesting that in the accompanying example we have identified a third allele at the *IGF2*-
10 linked QTL. The effects on muscle mass of the three alleles rank in the same order as the breeds in which they are found i.e. Piétrain pigs are more muscular than Large White pigs that in turn have higher lean meat content than Wild Boars.

15 There are good reasons to decide that *IGF2* is the causative gene for the now reported QTL. Firstly, there is a perfect agreement in map localization (Fig. 2). Secondly, it has been shown that *IGF2* is paternally expressed in mice, humans, and now in pigs, like the QTL.
20 There are several other imprinted genes in the near vicinity of *IGF2* in mice and humans (*Mash2*, *INS2*, *H19*, *KVLQT1*, *TAPA1/CD81*, and *CDKN1C/p57^{KIP2}*) but only *IGF2* is paternally expressed in adult tissues²². We believe that this locus provides a unique opportunity for molecular
25 characterization of a QTL. The clear paternal expression can be used to exclude genes that do not show this mode of inheritance. Moreover, the presence of an allelic series should facilitate the difficult distinction between causative mutations and linked neutral
30 polymorphism. We have already shown that there is no difference in coding sequence between *IGF2* alleles from Piétrain and Large White pigs suggesting that the causative mutations occur in regulatory sequences. An obvious step is to sequence the entire *IGF2* gene and its
35 multiple promoters from the three populations. The recent

report that a VNTR polymorphism in the promoter region of the insulin (*INS*) gene affects *IGF2* expression²³ suggests that the causative mutations may be at a considerable distance from the *IGF2* coding sequence.

- 5 The results have several important implications for the pig breeding industry. They show that genetic imprinting is not an esoteric academic question but need to be considered in practical breeding programs. The detection of three different alleles in Wild Boar, Large
- 10 White, and Piétrain populations indicates that further alleles at the *IGF2*-linked QTL segregate within commercial populations. The paternal expression of the QTL facilitates its detection using large paternal half-sib families as the female contribution can be ignored.
- 15 The QTL is exploited to improve lean meat content by marker assisted selection within populations or by marker assisted introgression of favorable alleles from one population to another.
-

Example 2: Piétrain x Large White intercrosses

Methods

Pedigree material: The pedigree material utilized to map

- 5 QTL was selected from a previously described Piétrain x Large White F2 pedigree comprising > 1,800 individuals^{6,7}. To assemble this F2 material, 27 Piétrain boars were mated to 20 Large White sows to generate an F1 generation comprising 456 individuals. 31 F1 boars were mated to
10 unrelated 82 F1 sows from 1984 to 1989, yielding a total of 1862 F2 offspring. F1 boars were mated on average to 7 females, and F1 sows to an average of 2,7 males. Average offspring per boar were 60 and per sow 23.

- 15 *Phenotypic information:* (i) *Data collection:* A total of 21 distinct phenotypes were recorded in the F2 generation^{6,7}. These included:

- five growth traits: birth weight (g), weaning weight (Kg), grower weight (Kg), finisher weight (Kg) and
20 average daily gain (ADG; Kg/day; grower to finisher period);
- two body proportion measurements: carcass length (cm); and a conformation score (0 to 10 scale; ref.6);
- ten measurements of carcass composition obtained by
25 dissection of the chilled carcasses 24 hours after slaughter. These include measurements of muscularity: % ham (weight hams/carcass weight), % loin (weight loin/carcass weight), % shoulder (weight
30 shoulder/carcass weight), % lean cuts (% ham + %loin + % shoulder); and measurements of fatness: average back-fat thickness (BFT; cm), % backfat (weight backfat/carcass weight), % belly (weight belly/carcass weight), % leaf fat (weight leaf fat/carcass weight), % jowl (weight jowl/carcass weight), and "% fat cuts" (% backfat + %
35 belly + % leaf fat + % jowl).
- four meat quality measurements: pH _{LD1} (*Longissimus dorsi* 1

hour after slaughter), pH _{LD24} (*Longissimus dorsi* 24 hours after slaughter), pH _{G1} (*Gracilis* 1 hour after slaughter) and pH _{G24} (*Gracilis* 24 hours after slaughter). (ii) *Data*

- 5 *processing*: Individual phenotypes were preadjusted for fixed effects (sire, dam, CRC genotype, sex, year-season, parity) and covariates (litter size, birth weight, weaning weight, grower weight, finisher weight) that proved to significantly affect the corresponding trait. Variables included in the model were selected by stepwise regression.

10

- Marker genotyping*: Primer pairs utilized for PCR amplification of microsatellite markers are as described¹⁹. Marker genotyping was performed as previously described²⁰. Genotypes at the *CRC* and *MyoD* loci were determined using conventional methods as described^{1,12}. The LAR test for the Igf2 SNP was developed according to Baron et al.²¹ using a primer pair for PCR amplification (5'-CCCCCTGAAGTGGAGGACGAGCAGCC-3'; 5'-ATCGCTGTGGGCTGGGTGGGCTGCC-3') and a set of three primers for the LAR step (5'-FAM-CGCCCCAGCTGCCCCCAG-3'; 5'-HEX-CGCCCCAGCTGCCCCCAA-3'; 5'-CCTGAGCTGCAGCAGGCCAG-3').

- Map construction*: Marker maps were constructed using the TWOPOINT, BUILD and CHROMPIC options of the CRIMAP package²². To allow utilisation of this package, full-sib families related via the boar or sow were disconnected and treated independently. By doing so, some potentially usable information was neglected, yielding, however, unbiased estimates of recombination rates.

30

QTL mapping: (i) *Mapping Mendelian QTL*: Conventional QTL mapping was performed using a multipoint maximum likelihood method. The applied model assumed one segregating QTL per

chromosome, and fixation of alternate QTL alleles in the respective parental lines, Piétrain (P) and Large White (LW). A specific analysis program had to be developed to account for the missing genotypes of the parental generation, resulting in the fact that the parental origin of the F1 chromosomes could not be determined. Using a typical "interval mapping" strategy, an hypothetical QTL was moved along the marker map using user-defined steps. At each position, the likelihood (L) of the pedigree data was computed as:

$$L = \sum_{g=1}^r \prod_{i=1}^n \sum_{G=1}^4 (P(G|M_i, \theta, \phi) P(y_i|G))$$

P or right chromosome P), there is a total of 2^r combinations for r F1 parents.

$$\prod_{i=1}^n n \text{ F2}$$

$\sum_{G=1}^4$ ith F2 offspring, over the four possible QTL genotypes:

P/P, P/LW, LW/P and LW/LW

$P(G|M_i, \theta, \phi)$: the marker genotype of the i th F2 offspring and its F1 parents, (ii) : the vector of recombination rates between adjacent markers and between the hypothetical QTL and its flanking markers, and (iii) θ the considered marker-QTL phase combination of the F1 parents.

Recombination rates and marker linkage phase of F1 parents are assumed to be known when computing this probability. Both were determined using CRIMAP in the map construction phase (see above).

$P(y_i|G) y_i$ of offspring i , given the QTL genotype under consideration. This probability is computed from the normal density function:

$$P(y_i|G) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(y_i - \mu_G)^2}{2\sigma^2}}$$

μ_G is the phenotypic mean of the considered QTL genotype (PP, PL, LP or LL) and σ^2 the residual variance σ^2 was considered to be the same for the four QTL genotypic classes.

- 5 The values of μ_{PP} , $\mu_{PL}=\mu_{LP}$, μ_{LL} and σ^2 maximizing L were determined using the GEMINI optimisation routine²³. The likelihood obtained under this alternative H_1 hypothesis was compared with the likelihood obtained under the null hypothesis H_0 of no QTL, in which the phenotypic means of the
- 10 four QTL genotypic classes were forced to be identical. The difference between the logarithms of the corresponding likelihoods yields a lodscore measuring the evidence in favour of a QTL at the corresponding map position.

- (ii) *Significance thresholds*: Following Lander & Botstein²⁴,
- 15 lodscore thresholds (T) associated with a chosen genome-wide significance level, were computed such that:

$$\alpha = (C + 9.21GT) \chi_1^2(4.6T)$$

C corresponds to the number of chromosomes (= 19), G corresponds to the length of the genome in Morgans (= 29),

- 20 and $\chi_1^2(4.6T)$ denotes one minus the cumulative distribution function of the chi-squared distribution with 2 d.f. Single point $2\ln(LR)$ were assumed to be distributed as a chi-squared distribution with two degrees of freedom, as we were fitting both an additive and dominance component. To account for the
- 25 fact that we were analysing multiple traits, significance levels were adjusted by applying a Bonferoni correction corresponding to the effective number of independent traits that were analyzed. This effective number was estimated at 16 following the approach described by Spelman et al.²⁵.
- 30 Altogether, this allowed us to set the lodscore threshold associated with an experiment-wise significance level of 5%

at 5.8. When attempting to confirm the identified QTL in an independent sample, the same approach was used, however, setting C at 1, G at 25cM and correcting for the analysis of 4.5 independent traits (as only six traits were analyzed in this sample). This yielded a lodscore threshold associated with a Type I error of 5% of 2.

(iii). *Testing for an imprinted QTL*: To test for an imprinted QTL, we assumed that only the QTL alleles transmitted by the parent of a given sex would have an effect on phenotype, the QTL alleles transmitted by the other parent being "neutral". The likelihood of the pedigree data under this hypothesis was computed using equation 1. To compute $P(y_i | G)$, however, the phenotypic means of the four QTL genotypes were set at $\mu_{PP} = \mu_{PL} = \mu_P$ and $\mu_{LP} = \mu_{LL} = \mu_L$ to test for a QTL for which the paternal allele only is expressed, and $\mu_{PP} = \mu_{LP} = \mu_P$ and $\mu_{PL} = \mu_{LL} = \mu_L$ to test for a QTL for which the maternal allele only is expressed. It is assumed in this notation that the first subscript refers to the paternal allele, the second subscript to the maternal allele. H_0 was defined as the null-hypothesis of no QTL, H_1 testing the presence of a Mendelian QTL; H_2 testing the presence of a paternally expressed QTL, and H_3 testing the presence of a maternally expressed QTL.

RT-PCR: Total RNA was extracted from skeletal muscle according to Chirgwin et al.²⁶. RT-PCR was performed using the Gene-Amp RNA PCR Kit (Perkin-Elmer) The PCR products were purified using QiaQuick PCR Purification kit (Qiagen) and sequenced using Dye terminator Cycle Sequencing Ready Reaction (Perkin Elmer) and an ABI373 automatic sequencer.

In example 2 we report the identification of a QTL with major effect on muscle mass and fat deposition mapping to porcine 2p1.7. The QTL shows clear evidence for parental imprinting strongly suggesting the involvement of the *Igf2* locus.

5 A Piétrain X Large White intercross comprising 1125 F₂ offspring was generated as described^{6,7}. The Large White and Piétrain parental breeds differ for a number of economically important phenotypes. Piétrains are famed for their exceptional muscularity and leanness⁸ (Figure 2), while Large
10 Whites show superior growth performance. Twenty-one distinct phenotypes measuring (i) growth performance (5), (ii) muscularity (6), (iii) fat deposition (6), and (iv) meat quality (4), were recorded on all F₂ offspring.

 In order to map QTL underlying the genetic differences
15 between these breeds, we undertook a whole genome scan using microsatellite markers on an initial sample of 677 F₂ individuals. Analysis of pig chromosome 2 using a ML multipoint algorithm, revealed highly significant lodscores (up to 20) for six of the 12 phenotypes measuring muscularity
20 and fat deposition at the distal end of the short arm of chromosome 2 (Figure 3a). Positive lodscores were obtained for the remaining six phenotypes, however, not reaching the genome-wide significance threshold ($\alpha = 5\%$). To confirm this finding, the remaining sample of 355 F₂ offspring was
25 genotyped for the five most distal 2p markers and QTL analysis performed for the traits yielding the highest lodscores in the first analysis. Lodscores ranged from 2.1 to 7.7, clearly confirming the presence of a major QTL in this region. Table 2 reports the corresponding ML estimates for
30 the three genotypic means as well as the corresponding residual variance.

 Bidirectional chromosome painting establishes a correspondence between SSC2p and HSA11pter-q13^{9,10}. At least

two serious candidate genes map to this region in man: the myogenic basic helix-loop-helix factor, *MyoD*, maps to HSA11p15.4, while *Igf2* maps to HSA11p15.5. *MyoD* is a well known key regulator of myogenesis and is one of the first myogenic markers to be switched on during development¹¹. A previously described amplified sequence polymorphism in the porcine *MyoD* gene¹² proved to segregate in our F₂ material, which was entirely genotyped for this marker. Linkage analysis positioned the *MyoD* gene in the SW240-SW776 (odds > 1000) interval, therefore well outside the lod-2 drop off support interval for the QTL (figure 1). *Igf2* is known to enhance both proliferation and differentiation of myoblasts *in vitro*¹³ and to cause a muscular hypertrophy when overexpressed *in vivo*. Based on a published porcine adult liver cDNA sequence¹⁴, we designed primer pairs allowing us to amplify the entire *Igf2* coding sequence with 222 bp of leader and 280 bp of trailer sequence from adult skeletal muscle cDNA. Piétrain and Large White RT-PCR products were sequenced indicating that the coding sequences was identical in both breeds and with the published sequence. However, a G A transition was found in the leader sequence corresponding to exon 2 in man (Figure 4). We developed a screening test for this single nucleotide polymorphism (SNP) based on the ligation amplification reaction (LAR), allowing us to genotype our pedigree material. Based on these data, *Igf2* was shown to colocalize with the SWC9 microsatellite marker (= 0%), therefore located at approximately 2 centimorgan from the most likely position of the QTL and well within the 95% support interval for the QTL (figure 1). Subsequent sequence analysis demonstrated that the microsatellite marker SWC9 is actually located within the 3' UTR of the *Igf2* gene. Combined with available comparative mapping data for the PGA and FSH loci, these results suggest the occurrence of an interstitial

inversion of a chromosome segment containing *MyoD*, but not *Igf2* which has remained telomeric in both species.

Igf2 therefore appeared as a strong positional allele having the observed QTL effect. In man and mouse, *Igf2* is known to be imprinted and to be expressed exclusively from the paternal allele in several tissues¹⁵. Analysis of skeletal muscle cDNA from pigs heterozygous for the SNP and/or SWC9, shows that the same imprinting holds in this tissue in the pig as well (Figure 4). Therefore if *Igf2* were responsible for the observed effect, and knowing that only the paternal *Igf2* allele is expressed, one can predict that (i) the paternal allele transmitted by F1 boars (P or LW) would have an effect on phenotype of F2 offspring, (ii) the maternal allele transmitted by F1 sows (P or LW) would have no effect on phenotype of F2 offspring, and (iii) the likelihood of the data would be superior under a model of a bimodal (1:1) F2 population sorted by inherited paternal allele when compared to a conventional "Mendelian" model of a trimodal (1:2:1) F2 population. The QTL mapping programs were adapted in order to allow testing of the corresponding hypotheses. H_0 was defined as the null-hypothesis of no QTL, H_1 as testing for the presence of a Mendelian QTL, H_2 as testing for the presence of a paternally expressed QTL, and H_3 as testing for the presence of a maternally expressed QTL. Figure 3 summarizes the obtained results. Figure 3a, 3b and 3c respectively show the lodscore curves corresponding to $\log_{10} (H_2/H_0)$, $\log_{10} (H_3/H_0)$ and $\log_{10} (H_2/H_1)$. It can be seen that very significant lodscores are obtained when testing for the presence of a paternally expressed QTL, while there is no evidence at all for the segregation of a QTL when studying the chromosomes transmitted by the sows. Also, the hypothesis of a paternally expressed QTL is significantly more likely ($\log_{10} (H_2/H_1) > 3$) than the hypothesis of a "Mendelian" QTL

for all examined traits. The fact that the same tendency is observed for all traits indicates that it is likely the same imprinted gene that is responsible for the effects observed on the different traits. Table 2 reports the ML phenotypic means for the F2 offspring sorted by inherited paternal QTL allele. Note that when performing the analysis under a model of a mendelian QTL, the Piétrain and Large White QTL alleles appeared to behave in an additive fashion, the heterozygous genotype exhibiting a phenotypic mean corresponding exactly to the midpoint between the two homzygous genotypes. This is exactly what one would predict when dealing with an imprinted QTL as halve of the heterozygous offspring are expected to have inherited the P allele from their sire, the other halve the LW allele.

These data therefore confirmed our hypothesis of the involvement of an imprinted gene expressed exclusively from the paternal allele. The fact that the identified chromosomal segment coincides precisely with an imprinted domain documented in man and mice strongly implicates the orthologous region in pigs. At least seven imprinted genes mapping to this domain have been documented (*Igf2*, *Ins2*, *H19*, *Mash2*, *p57^{KIP2}*, *KvLQTL1* and *TDAG51*) (ref. 15 and Andrew Feinberg, personal communication). Amongst these, only *Igf2* and *Ins2* are paternally expressed. While we cannot exclude that the observed QTL effect is due to an as of yet unidentified imprinted gene in this region, its reported effects on myogenesis *in vitro* and *in vivo*¹³ strongly implicate *Igf2*. Particularly the muscular hypertrophy observed in transgenic mice overexpressing *Igf2* from a muscle specific promotor are in support of this hypothesis (Nadia Rosenthal, personal communication. Note that allelic variants of the *INS* VNTR have recently been shown to be associated

with size at birth in man¹⁶, and that the same VNTR has been shown to affect the level of *Igf2* expression¹⁷.

The observation of the same QTL effect in a Large White x Wild Boar intercross indicates the existence of a series of
5 at least three distinct functional alleles. Moreover, preliminary evidence based on marker assisted segregation analysis points towards residual segregation at this locus within the Piétrain population (data not shown). The occurrence of an allelic series might be invaluable in
10 identifying the causal polymorphisms which - based on the quantitative nature of the observed effect - are unlikely to be gross gene alterations but rather subtle regulatory mutations.

The effects of the identified QTL on muscle mass and fat
15 deposition are truly major, being of the same magnitude of those reported for the *CRC* locus^{6,7} though apparently without the associated deleterious effects on meat quality. We estimate that both loci jointly explain close to 50% of the Piétrain versus Large White breed difference for muscularity
20 and leanness. Understanding the parent-of-origin effect characterizing this locus will allow for its optimal use in breeding programs. Indeed, today half of the offspring from commercially popular Piétrain x Large White crossbred boars inherit the unfavourable Large White allele causing
25 considerable loss.

The QTL described in this work is the second example of a gene affecting muscle development in livestock species that exhibits a non-mendelian inheritance pattern. Indeed, we have previously shown that the callipyge locus (related to the
30 qualitative trait wherein muscles are doubled) is characterized by polar overdominance in which only the heterozygous individuals that inherit the CLPG mutation from their sire express the double-muscling phenotype⁵. This

demonstrates that parent-of-origin effects affecting genes underlying production traits in livestock might be relatively common.

5 Example 3:

Generating a reference sequence of IGF2 and flanking loci in the pig.

- 10 The invention provides an imprinted QTL with major effect on muscle mass mapping to the IGF2 locus in the pig, and use of the QTL as tool in marker assisted selection. To fine tune this tool for marker assisted selection, as well as to further identify a causal mutation, we have further generated
- 15 a reference sequence encompassing the entire porcine IGF2 sequence as well as that from flanking genes.

To achieve this, we screened a porcine BAC library with IGF2 probes and identified two BACs. BAC-PIGF2-1 proved to

20 contain the INS and IGF2 genes, while BAC-PIGF2-2 proved to contain the IGF2 and H19 genes. The NotI map as well as the relative position of the two BACs is shown in Figure 5. BAC-PIGF2-1 was shotgun sequenced using standard procedures and automatic sequencers. The resulting sequences were assembled

25 using standard software yielding a total of 115 contigs. The corresponding sequences are reported in figure 6. Similarity searches were performed between the porcine contigs and the orthologous sequences in human. Significant homologies were detected for 18 contigs and are reported in Figure 7.

- 30 For BAC-PIGF2-2, the 24 Kb NotI fragment not present in BAC-PIGF2-1 was subcloned and sequenced using the EZ::TN transposon approach and ABI automatic sequencers. Resulting

sequences were assembled using the Phred-Phrap-Consed program suit, yielding seven distinct contigs (figure 8). The contig sequences were aligned with the corresponding orthologous human sequences using the compare and dotplot programs of the GCG suite. Figure 9 summarizes the corresponding results.

Example 4: Identification of DNA sequence polymorphisms in the IGF2 and flanking loci.

- 10 Based on the reference sequence obtained as described in Example 1, we resequenced part of the IGF2 and flanking loci from genomic DNA isolated from Piétrain, Large White and Wild Boar individuals, allowing identification of DNA sequence polymorphisms such as reported in figure 10.

15

Legends to the figures

Fig. 1: Test statistic curves obtained in QTL analyses of
5 chromosome 2 in a Wild Boar/Large White intercross. The graph
plots the F ratio testing the hypothesis of a single QTL at a
given position along the chromosome for the traits indicated.
The marker map with the distances between markers in Kosambi
centiMorgan is given on the X-axis. The horizontal lines
10 represent genome-wide significant ($P < 0.05$) and suggestive
levels for the trait lean meat in ham; similar significance
thresholds were obtained for the other traits.

Figure 2: Piétrain pig with characteristic muscular
15 hypertrophy.

Figure 3: Lodscore curves obtained in a Piétrain x Large
White intercross for six phenotypes measuring muscle mass and
fat deposition on pig chromosome 2. The most likely positions
20 of the *Igf2* and *MyoD* genes determined by linkage analysis
with respect to the microsatellite marker map are shown. H_0
was defined as the null-hypothesis of no QTL, H_1 as testing
for the presence of a Mendelian QTL, H_2 as testing for the
presence of a paternally expressed QTL, and H_3 as testing for
25 the presence of a maternally expressed QTL. 3a: $\log_{10}(H_1/H_0)$,
3b: $\log_{10}(H_2/H_0)$, 3c: $\log_{10}(H_3/H_0)$

Figure 4: A. Structure of the human *Igf2* gene according to
ref. 17, with aligned porcine adult liver cDNA sequence as
30 reported in ref. 16. The position of the nt241(G-A)
transition and Swc9 microsatellite are shown. B. The
corresponding markers were used to demonstrate the
monoallelic (paternal) expression of *Igf2* in skeletal muscle

and liver of 10-week old fetuses. PCR amplification of the *nt421(G-A)* polymorphism and *Swc9* microsatellite from genomic DNA clearly shows the heterozygosity of the fetus, while only the paternal allele is detected in liver cDNA (*nt421(G-A)* and *Swc9*) and muscle cDNA (*Swc9*). The absence of RT-PCR product for *nt421(G-A)* from in fetal muscle points towards the absence of mRNA including exon 2 in this tissue. Parental origin of the foetal alleles was determined from the genotypes of sire and dam (data not shown).

10

Figure 5: A NotI restriction map showing the relative position of BAC-PIGF2-1 (comprising INS and IGF2 genes), and BAC-PIGF2-2 (comprising IGF2 and H19 genes).

15 Figure 6: Nucleic acid sequences of contig 1 to contig 115 derived from BAC-PIGF2-1 which was shotgun sequenced using standard procedures and automatic sequencers.

Figure 7: Similarity between porcine contigs of figure 6 and orthologous sequences in human.

20

Figure 8 Nucleic acid sequences of contig 1 to contig 7 derived from BAC-PIGF2-2, (the 24 Kb NotI fragment not present in BAC-PIGF2-1) which was subcloned and sequenced using the EZ::TN transposon approach and ABI automatic sequencers.

25

Figure 9: Similarity between porcine contigs of figure 8 and orthologous sequences in human.

30

Figure 10: DNA sequence polymorphisms in the IGF2 and flanking loci from genomic DNA isolated from Piétrain, Large White and Wild Boar individuals.

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Table 1 Summary of OTL analysis for pig chromosome 2 in a Wild Boar/Large White Intercross¹

| Trait | <i>L^P/L^M</i> | F ratio ² | Imprinting | Map position ¹ | Percent of F ₂ variance ¹ | Least squares means ³ | <i>L^P/W^M</i> | <i>W^P/L^M</i> | <i>L^P/W^M</i> |
|----------------------------------|--|----------------------|------------|---------------------------|---|----------------------------------|------------------------------------|------------------------------------|------------------------------------|
| Body composition traits | | | | | | | | | |
| 10 | Lean meat in ham, % | 24.4*** | 19.1*** | 0 | 30.6 | 63.6 ^a | 64.2 ^a | 66.4 ^b | 67.3 ^b |
| | Lean meat mass in ham, kg | 18.1*** | 16.8*** | 1 | 24.3 | 4.69 ^a | 4.72 ^a | 4.94 ^b | 5.02 ^b |
| | Lean meat + bone in back, % | 12.2** | 9.6** | 0 | 17.4 | 66.3 ^a | 66.7 ^a | 69.3 ^b | 70.8 ^b |
| | Longissimus muscle area, cm ² | 10.3** | 4.8* | 1 | 15.4 | 31.9 ^a | 33.0 ^a | 34.5 ^b | 35.2 ^b |
| Fatness traits | | | | | | | | | |
| 15 | Average back fat depth, mm | 7.1* | 8.7** | 0 | 10.4 | 27.2 ^a | 27.7 ^a | 25.5 ^b | 24.7 ^b |
| Weight of internal organs | | | | | | | | | |
| 20 | Heart, gram | 9.7** | 11.4*** | 0 | 14.4 | 226 ^a | 225 ^a | 238 ^b | 244 ^b |
| | Meat quality traits | | | | | | | | |
| | Reflectance value, EEL | 5.7 | 6.1* | 1 | 8.1 | 18.6 ^a | 18.4 ^a | 21.8 ^b | 19.7 ^b |

*P<0.05; **P<0.01; ***P<0.001

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Table 1, continued

- 1 Only the traits for which the QTL peak was in the *IGF2*
5 region (0-10 cM) and the test statistic reached the nominal
significance threshold of $F=3.9$ are included.
- 2 "QTL" is the test statistic for the presence of a QTL under
a genetic model with additive, dominance, and imprinting
effects (3 d.f.) while "Imprinting" is the test statistic for
10 the presence of an imprinting effect (1 d.f.), both obtained
at the position of the QTL peak. Genome-wise significance
thresholds, estimated by permutation, were used for the QTL
test while nominal significance thresholds were used for the
Imprinting test.
- 15 3 In cM from the distal end of 2p; *IGF2* is located at 0.3 cM.
4 The reduction in the residual variance of the F_2 population
effected by inclusion of an imprinted QTL at the given
position.
- 5 Means and standard errors estimated at the *IGF2* locus by
20 classifying the genotypes according to the population and
parent of origin of each allele. *W* and *L* represent alleles
derived from the Wild Boar and Large White founders,
respectively; superscript *P* and *M* represent a paternal and
maternal origin, respectively. Figures with different letters
25 (superscript a or b) are significantly different at least at
the 5% level, most of them are different at the 1% or 0.1%
level.
-

Table 2 Maximum likelihood phenotypic means for the different F2 genotypes estimated under (i) a model of a mendelian QTL, and (ii) a model assuming an imprinted QTL.

| Traits | Mendelian QTL | | | | Imprinted QTL | | |
|-------------|---------------|--------------|-------------|------|----------------|---------------|------|
| | $\mu_{LM/LM}$ | $\mu_{LM/P}$ | $\mu_{P/P}$ | R | $\mu_{PAT/LM}$ | $\mu_{PAT/P}$ | R |
| BFT (cm) | 2.98 | 2.84 | 2.64 | 0.27 | 2.94 | 2.70 | 0.27 |
| % ham | 21.10 | 21.56 | 22.15 | 0.83 | 21.23 | 21.9 5 | 0.83 |
| % loin | 24.96 | 25.53 | 26.46 | 0.91 | 25.12 | 26.1 4 | 0.93 |
| % lean cuts | 65.02 | 65.96 | 67.60 | 1.65 | 65.23 | 67.0 5 | 1.67 |
| % backfat | 6.56 | 6.02 | 5.33 | 0.85 | 6.43 | 5.56 | 0.85 |
| % fat cuts | 28.92 | 27.68 | 26.66 | 1.46 | 28.54 | 26.9 9 | 1.49 |

Comprises/comprising and grammatical variations thereof when used in this specification are to be taken to specify the presence of stated features, integers, steps or components or groups thereof, but do not preclude the presence or addition of one or more other features, integers, steps, components or groups thereof.

55

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A method for selecting a domestic animal for having desired genotypic properties comprising testing said animal for the presence of a parentally imprinted quantitative trait locus (QTL), wherein the method further comprises
5 testing a nucleic acid sample from said animal for the presence of a parentally imprinted QTL, and wherein said QTL is related to the potential muscle mass and/or fat deposition of said animal.
2. A method according to claim 1 wherein said QTL comprises at least a part of an insulin-like growth factor-2 (IGF2) gene.
- 10 3. A method according to claim 1 or 2 wherein in the pig said QTL comprises a marker characterised as nt241 (G-A) or as Swc9.
4. A method according to any one of claims 1 to 3 wherein a paternal allele of said QTL is predominantly expressed in said animal.
5. A method according to any one of claims 1 to 3 wherein a maternal allele
15 of said QTL is predominantly expressed in said animal.
6. Use of an isolated and/or recombinant nucleic acid comprising a parentally imprinted quantitative trait locus (QTL) derived from at least one chromosome or functional fragment derived thereof in the method of any one of claims 1 to 5.
7. Use according to any claim 6 wherein said QTL is related to the potential
20 muscle mass and/or fat deposition of said animal.
8. Use according to claim 6 wherein said QTL comprises at least a part of a insulin-like growth factor-2 (IGF2) gene.
9. Use according to any one of claims 6 to 8 wherein a paternal allele of said QTL is capable of being predominantly expressed.

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10. Use according to any one of claims 6 to 9 wherein a maternal allele of said QTL is capable of being predominantly expressed.
11. Use according to any one of claims 6 to 10 to select a breeding animal or animal destined for slaughter for having desired genotypic or potential phenotypic properties, wherein said properties are related to muscle mass and/or fat deposition.
12. Use according to claim 11 to select a pig.
13. Use according to claim 12, wherein the pig is homozygous for an allele at a paternally Imprinted QTL, preferably located at a *Sus scrofa* chromosome 2 mapping at around position 2pl. 7, wherein said QTL is related to the potential muscle mass and/or fat deposition of said pig and/or wherein said QTL comprises at least a part of a Insulin-like growth factor-2 (IGF2) allele.
14. Use of the isolated and/or recombinant nucleic acid as defined in any one of claims 6 to 9 to develop a transgenic animal.
15. Use according to any one of claims 12 to 14, wherein the animal is a male.
16. Sperm or an embryo derived from an animal developed according to claim 14.
17. Use of a sperm or an embryo according to claim 16, in breeding animals destined for slaughter.
18. A method for selecting a domestic animal for having desired genotypic properties substantially as hereinbefore described with reference to the Examples.

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19. Use of an isolated nucleic acid substantially as hereinbefore described with reference to the examples.

DATED this 30th day of November, 2004

UNIVERSITY OF LIEGE, MELICA HB AND SEGHERSGENTEC N.V.

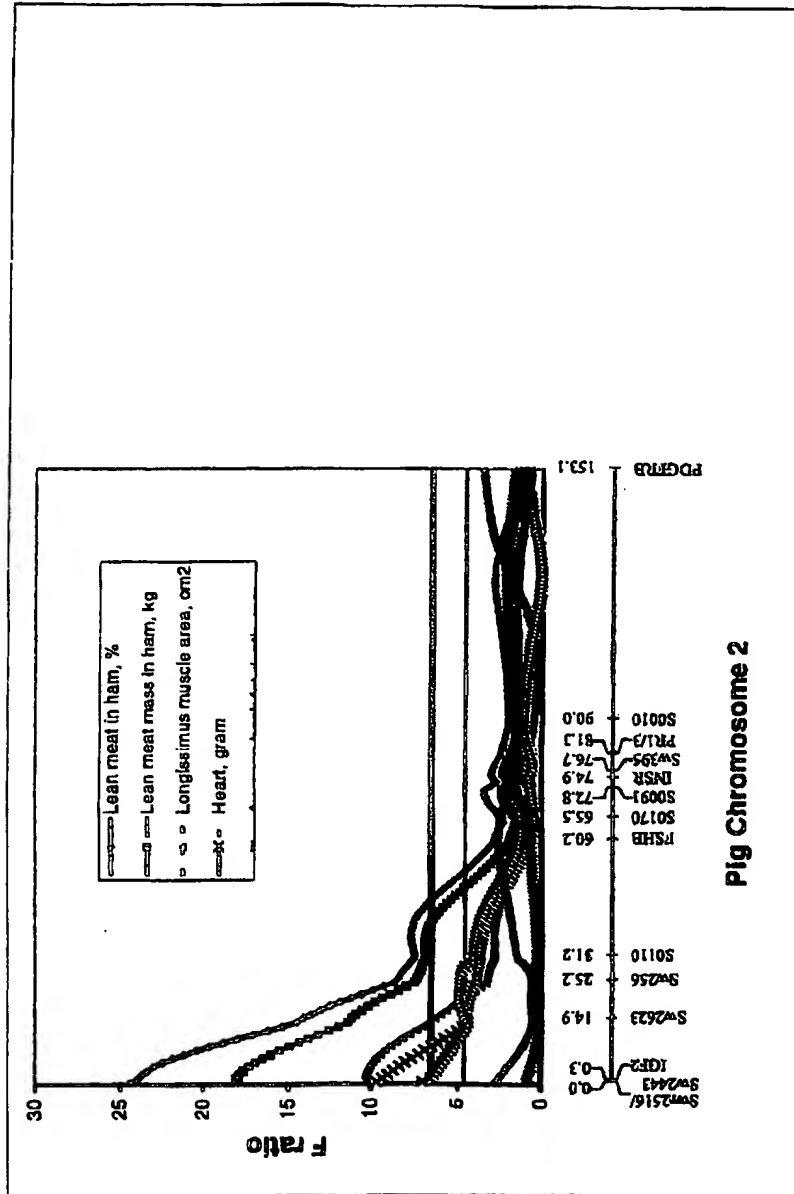


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290 BURWOOD ROAD
HAWTHORN VICTORIA 3122
AUSTRALIA

P19791AU00



FIGURE 1



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FIGURE 2



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FIGURE 3A

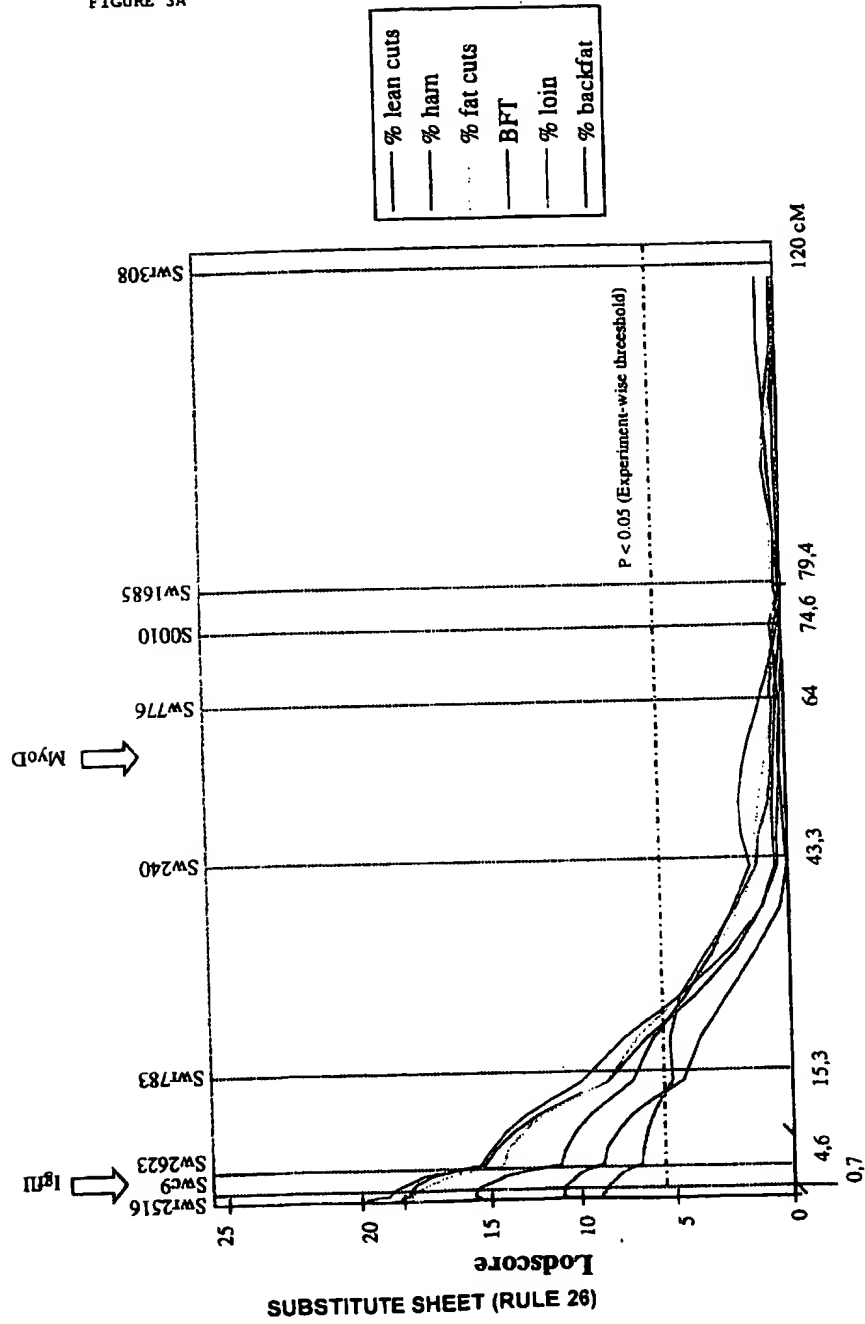


FIGURE 3B

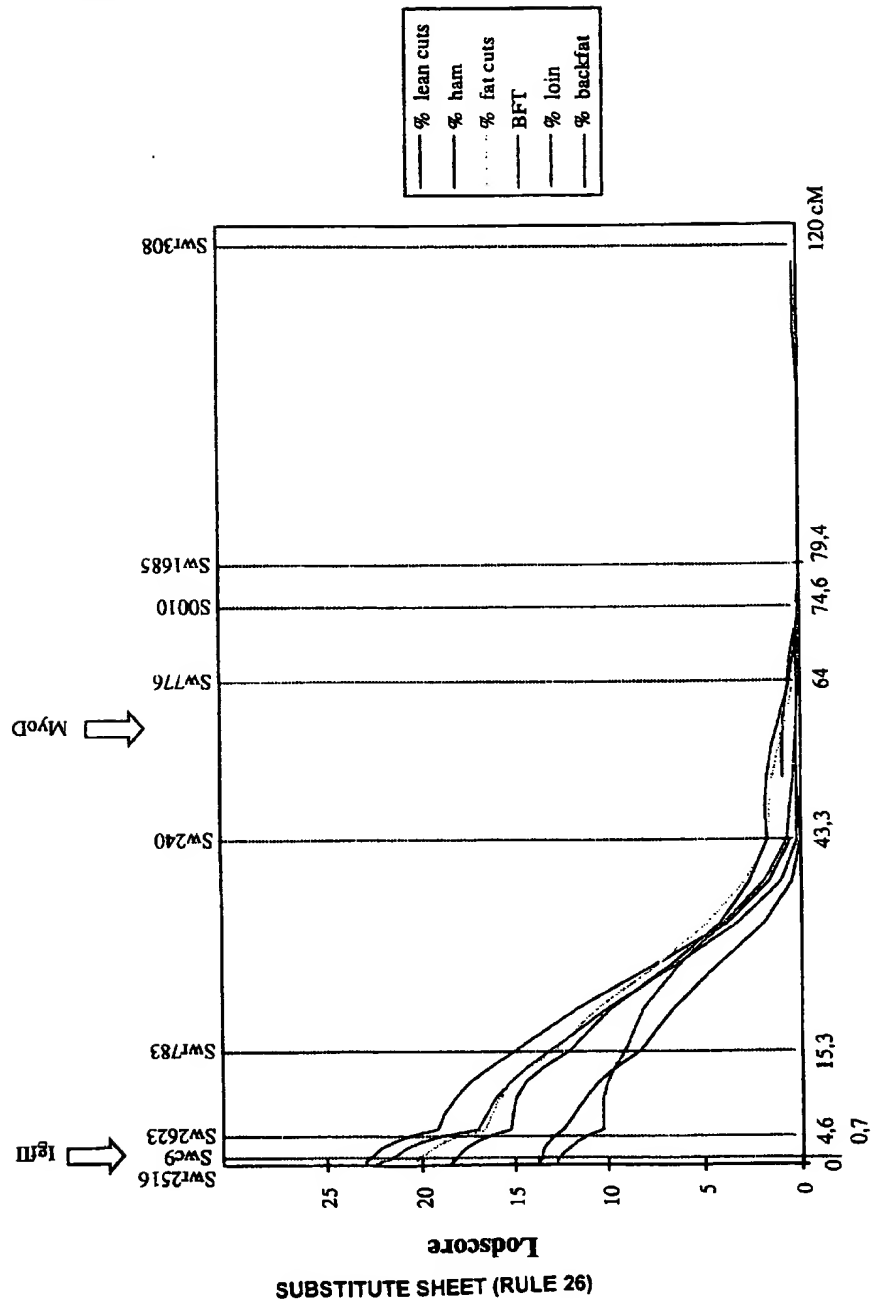


FIGURE 3C

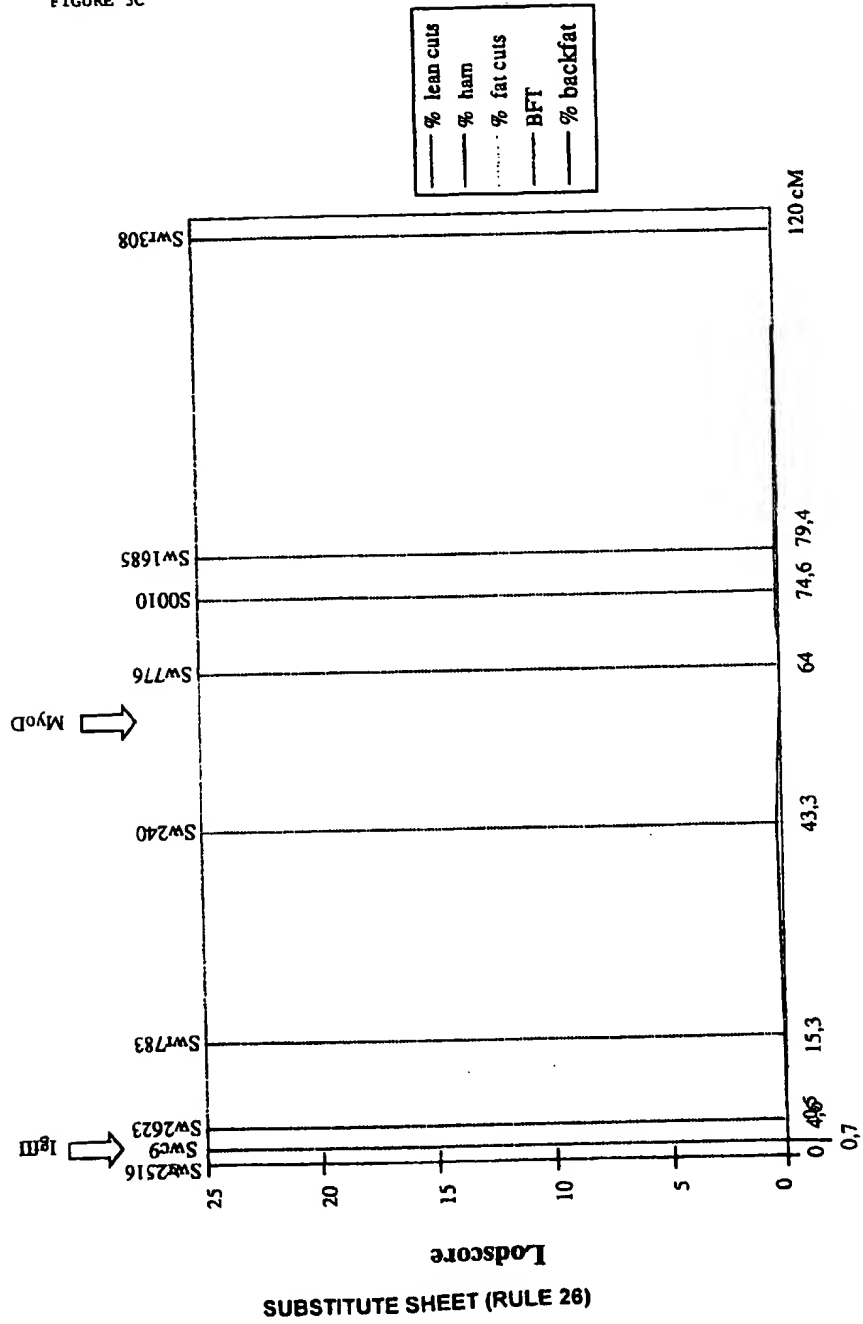
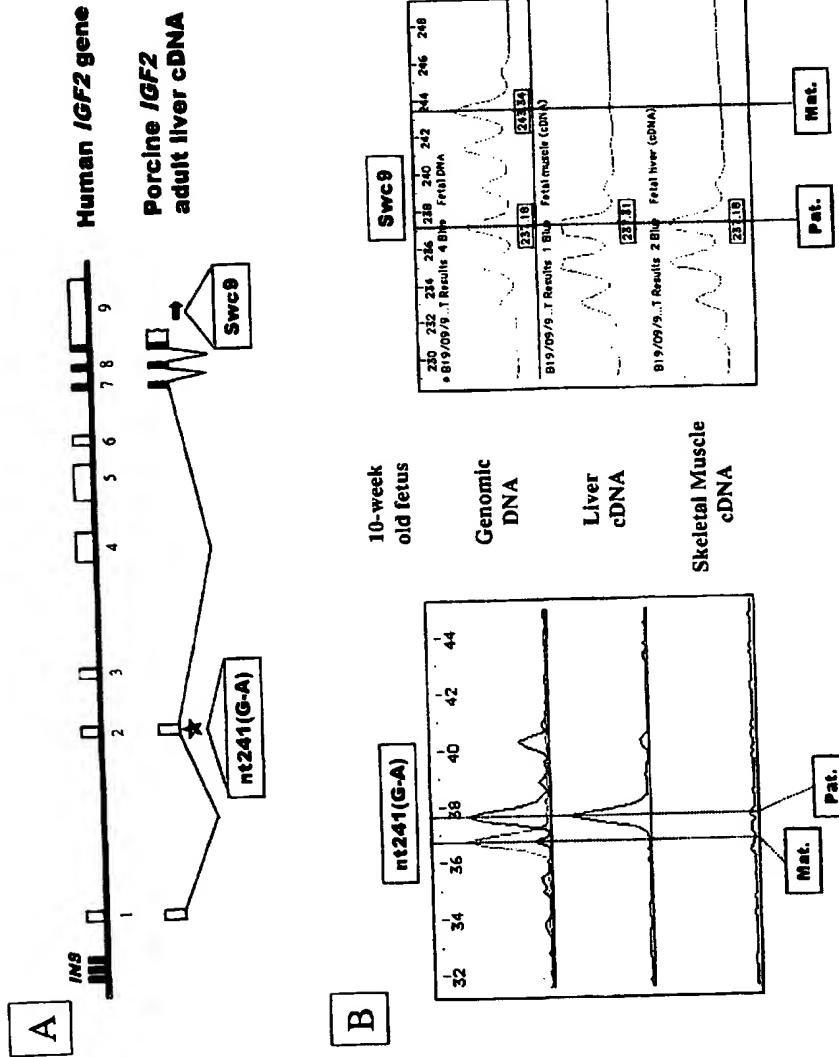
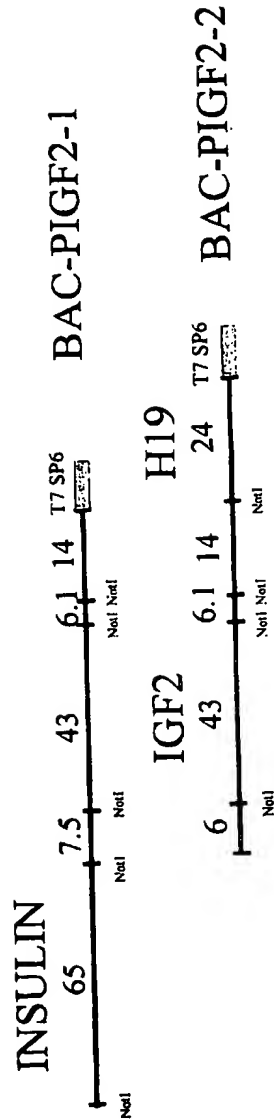


FIGURE 4



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FIGURE 5



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FIGURE 6

Contig 1 (500 bp)

GGGTGGGACGCTTCCTCCAGACCCGAGGAGGCCAAGTTCCCTGGCCCTGCCACCCAGGGCCAGCTGAAGC
AGGTGAGAGACACCCGCTCTCTGCTCCCTGTCACCTAACCCACAGGCCGGGGCCAGGGACACAGGCCACA
TGGCATCTCCCCCATGCCCTGCCCAAGGCGCCAGCAGGTGAGGCTGGAGCAGAGTCTGGGTCTCGGG
CCAGACCGAGGGCAGGACAGCTGGGCATCTGTCTACAGTCCCGCGCTTTGTGGGAGGGCGGAGGCTC
ATCCAAGACGCCCAAGGAACCGGAGAGGCGGAGGCGCGGCTGCCGCGTCCAGGCCGGGGAGGCGCTTG
AAGTGGGGGCGCTTGGCGAGCGGGAGCGGAAGCCCTGCTCAACCTGCTTTCAACCTGAGGGCCACCAAGCC
CCCCCTCGCTGTCCGGTCCCTGAAAAAATTTAGGTGAGGGGGGGGCCAGGGCTCCCCGGG

Contig 2 (943 bp)

TGCTCTCACACCCCGGGCGGGCTGCTTTGGGGCCATCTCCCATGGGCCACACCCACTCTGGCCTTC
ACACCTGCGCTTCTGGGAAGTCTCTGGTTCCCAAGGAAGTTTCTGAGCTGGACAAGTGCCACCACTGG
TCACCAAGTTCGATCTGAGCTGGACCTGGACCAACCCGGTGAGCCGGTGCTCCCTCCCCGGCGCCATGTC
TCCCATCCCCAGGGGTGTCCCACTAGGGCGGGGACTGGGCGTGAACCCCGGGTTGGGACGGATGTTGGC
CTGCTGTGTGGCTCTGGCGGAACAGAGAGGCTGGTGGTGCCACCCAGGGCCCCCGCGATGACACGG
GCCGCGTCTGGGCTGGGCGGGCAGGGCGGCCAGGC
AGGGCAGCCTCCGATGGCGTCCCGGCTGTACACAGGCTTCTCGGACCAAGTTGACCGCCAGCGCAGGAAGC
TGATTGGCCAGATCGCCTTCAGTACAGCCAGTAAGTCCCTCCAGGGCCTCAGCTGGGGGCCAGACCTCAG
CCTGGGCGCTCAGGCCAGACCTGGGGGTGGAGGAAGGGAGGTTGCTTTGTACCAACGCCACCACTTCACT
GTACCATGGTACAGCACTCTGGGTCCCAATACAGCTGAGGAACTGGGGCAGAGTGGTTAAGCATCT
TGCTGAAGCCACAGCTGGCGGAGCATTTGGCCCGGCCCTCTGCGGCTCCACACCTGCTCCCTGAGGG
GCCCGGGACTGACAGCTGTCCCTCTCTCAGAGGTG
ACCCATTTCCTCCCGTGGAGTACACAGCCAGGAGATTGCCACCTGGTGAGGCCCTGTGACAGCGCTGGGAG
GGCGCGGAGTGGGGGAAGGACAGGAAGCTCAGAATTCCGCGTGGAACGTGGTGGCTCTATCATGA

Contig 3 (1500 bp)

GGGGAGGGGATGCTCAGACCCGCTCTGGGAAGAAGAGAGCCTCAGAAGAAATCCCTTCCCAAGGGTCACGCGG
TGGAGCCAGGGGCCCGCTAGGGGCCGATTCCACAGCTCGTGCTGCCACCTGCTGGCGCTCCAGGAACCTGC
GGAGGCGGTGGGGCCCTGGATGGGTCCGCGAGTGGGCTCGCAGGAGACCCCTGGAGGGGCTGCGGACACCC
AGCTGCCACTCACAAGGTGCCAAGCGCGGTGGCAATGGGCTGAGCCTCTCCCCCTCTCTCTCCGAGGA
CATTGGCCTCGCATCCCTGGGGGTCTCGGACGAGGAATGAGAAGCTGTCCACGGTGGGTTTCTCCCCCTGC
AGGGCCCTGGGTCCAGCCAGGCCCTCTCTGTCACAA
GGGGTGTCTGCTCAGCTGTGACCGCCCGGAGCCTGGATCGGTTCTGCTGGGTGGGCGGTGCCCGGGCCA
CGGGCAGCAGGGGACGCGGTGCGGGCCCGAGCCGTGTCTGAGCCCTTGGCGCTGTCCCAACAGCTGTAC
TGGTTACGGTGGAGTTTGGGCTCTGCAACAGACGCGGAGGTGAAGCCCTACGGGGCTGGGCTGTCTGCT
CCTACGGGGAGCTCTGGTGGGCTCCCCACGCGCTGGGCGCTGGGTCCCCGGGGAGGTGACCCCTGCGG
TGCTTGTGGATTCCAGCTCTCGGAGGCTGGAGCGAGGGGCTGCCCTCTGGGGCACCAGAAAGCTGGT
TGCGCCCTCTCCACACACTGTGCTGGGCCCTG
GGGGGACCCCTGCTGGGGATGTGGGTGCACAGCCAGGGGCCACAGGGAGTCAGGACAGGGGCTCCCTTCCC
TCGGGTCCCTGAGACCCCTGGCTTCCCGCAGCACTCCCTGTCCGAGGAGCCCGAGATCCGGCCCTTCGACCC
CGACCGCGGGCGGTGCAGCCCTACAGGACAGACCTACAGCCCGTCTACTTCTGTCTGAGAGTTTCAGT
GACGCCAAGGACAAGCTCAGGTGGGCGGGGCCCGGGGCCCAACTGGAGGATCCAGCTGACGCCCCGCC
TATGAGCCATTTCAGCAGAGGGAGCTGCTGCGGACCCACCGTCACAACCCCTTCCACAGCTGGAACC
CCAGAAAGCTCGGAGGGGGACCTGCAGGGCTG
TGGCCAGGTCAAGGCAGGTGAGGCCAGGCTTTAGGGGTGAAGTCTGACTTTGTAGAGGGGGTGCAGGGT
CCTTCCAGCTCTCCCTCCGAGCAGCTGGGGCGGGCGGGGTGCGATGAAGGCAGAGATGACGCGAGCC
ACCCGTTACCTCAGGAGGCGCTCTGTCCAGCAGGGTCTGTGTGTCACAGGGAACTGAGGCCCCAGG
TGTGTGTGTGGGGGGGTGATTCTCACACACAAGCTTAGGGACAGGGACATAAGGCGCTCTCAGGCGACAG
TCTGGAGG

Contig 4 (3024 bp)

TTAANTCCANGTTGGCCCGACAAGTTTCCCCATTTGAAAAGGGGCCAGTTAAGCCCCAACNCAATTAATTGG
AAGTTAGCTCCCTCATTAGGCTCCCCAGNCTTTACNCTTATGTTCCGGTTCGTATTTTGTGGGAATTGTA
GCGGATACAATTTCTCTCAAGNAACCAGCTATGCCATGATTACGCGGTACAGTAGTTCATCAGTCCCCCGG
CCCATGGGACAGCGAAGGGAACAGTATGTCGTGGGGCCGGGTCTAAAGGGGTACACACAGGGAGGGGAGG
GGCTCCAGGAGGCGGGCACTGAGCGGTACCTGGTGGGGGAGGTGGTGGGGCACACCCAGGAGTCTGTG
CCCCCCCCCTCCCGCGTGGACATGAGAAGCAGGGGCCAGCTGCGGGTCTGAGTTCAGGCCCCCCCC
CAGCCCCCCCCCAGCGCTTCAGAGCATCTGCGGGCTCAGGGATGGACCGGGGTCTGCRGGCAGGTGCTCTC
TCGCGCCCCACTCCCTGGGCTATAACGTGGAAGATGGGCCCCAAGCCCGGCGGTTTGGCCCTTGTCCCCAG
CCAGTGGGACAGCTGGCCCTCAGGCCCTCGTTAAGACTTAATGACCTCAAGGCCCCAGAGGCGCTGAT
GACCCACGGAGATGATCCCGAGGCTGCGACAGGGAATGATCCAGAAGTGCCACCTCAGCCCCAGGCCA

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FIGURE 6, CONTD.

TCTGCCACCCACCTGGAGGCCCTCAGGGGCCGGGGCGGGGGGCGAGGCGCTATAAAGCCGGCCGGGGCCAGC
 CGCCCCAGCCCTCTGGGAOCAGCTGTGTTCACAGGCCACGGCAAGCAGTCTGTCCCCCTGGGCTCCCGTC
 AGCTGGGTCTGGGCTGTCTGTCTGGGGCCAGGGCATCTCGGCAGGAGGACGTGGGCTCCTCTCTCGGAGCCCT
 TGGGGGGTGGGCTGTGTGGGGGTGCAGGTGCCCTGGCTGGCCCTCAACGCCGCCCTCCCCAGGTCTCAC
 CCCCCCATGGCCCTGTGCACGGCCCTCTGCCCTGTCTGCCCTGTCTGGCSCTCTGGGGGCCCGCCCGGC
 CCAGGCCCTCTGAACACAGCACTGTGGCCCTCCCACTTGTGGAGGGCGCTGTACCTGGTGTGGGGGAGCGC
 GGCTTCTCTACACGCCCAAGGCCCTGGGAGGGCGGAGAACCTCAGGGTGAGCCGAGGGGGYGTCCCGGA
 GCGGTGGGGGAGTTTTAAGGAGGAAATTGGTAAAGTGACCAACTCCCTGGGAGCTGAGCCAGAGACAC
 CCTCCACGCCCYGGTCCCGCTCGAGAAGCCCTTCCCTCCCTCCCTCCG
 AGGGGGCTCAGGGAGGAATCTTACGGAGTCAAGGCCGGGTGCCGTGGTCTCCGAGTGACATGGCCGTGGT
 GTCCCTCTGCGGCCACATGCCCTGAGAGAWGCCCATCCCCCTGGGAGGGGGCCCGTGCCTGGGAGGC
 GCGGGAGGCCAGGACCGGTGGCTGTCTGGCTTCCACTCAGGGGTGGGGGGGTGGGGGTGGCTGTCT
 GTGTGACCGGCTCTCCCGCAGCAGGTGTGGCTGGAGCTGGGGGAGCCCTGGGGGGCTGCAGGCCCTGGCG
 TGGAGGGGCCCGCAGAACCTGGCATCTGTGGAGCAGTGTGCACCACTCTGTTCCTCTACCACTGGA
 GAACACTGCAACTAGGGCGCCCTCAGGGGGCTGTCTGCCCGCACCCCAAAAGCCAAATAAGTCTGAA
 TGAGCCCGGGCGAGTCTGTGGTCTGTGGCTGGGGGGGGGGCCCTGGTGGGGAGGGGCCAGAGGCTGT
 GGGGGGCTGTCTGCGACCCCTCTCTGTCTCTCGCCACATCGGCTGTCTAAGCTTCTCCACATGCACTCGGT
 GCGCACAGCACTGGCCAGCGGGGACAGGGCCAGGGCAGGGCCCTTCAATGTGGCGAGCTCTGGTTTC
 AGGGCTCCAGACACCCCTCTGGGTGCCACTGTCTGCACAGGGTCACTCTGAGGGTCACAGGGCACCCACC
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 CCCCCGGGACCAAGACTTGGCCAGCTGCCAGTCTGCCAGTCTGCCAGGCCAAACCAATCTGCACCTTGTCTGAAGTTC
 ACCCGGGCAGCACTGGGGGGGGCGGGCTTAGAGCTGGGGCGCCGGGCCAGGGACTGCACACCCCGCAG
 AGGTGGGCTGTAGGGGTGGCAGCAGGTCTCTGGCTGGGACCCAGCCAGCTGGGCGAGTCACTCTCAACAG
 AGGTCTCACTGTGTGTCTCTCCCTCCCGCAGCCACACAGACACCCCTGGGGAGAGTCAAGGCCCGGCA
 GGCCCCCGCCCTGGAGAGGAGGCCAGGGCTGGGCGGGGTGGCGGGCCGACACTGCAACCCGGAAGGGGG
 TAGCGGGCTGGGATGAGTGGCGAGCTGTCCATGGGAGCACCCAGCGGCCCATTTGGCACAGTACAGCGAGGG
 GCACCTGCAGCAGCTGAGGTACGTGGGGTCCCGGAGTGGTGTGTCTGGCTGCCCTCTGGGAGGAGCGGG
 CTGAGCTTGTGGTCTGCCAACAGGAGACCCGTGACCACTCTGTCTCTCCCTCCCGCCAGGGCCAGGCT
 GACTCTTTGGGACTCGGGGGCTGAGCGGCCCACTGCGAGGACTCACGGGTGTGGGTCTCTGGGTGAG
 TGGGGGCTTGGGAGAGGCTCACTTGTCTGGTGGGTGGGAAAGGCTGAGAGTCATGGTGTGACAGCGCCCTC
 GGCTGCGGGGTGGGGGTCTCCCTTCTCCCGAGCCAGATCCCGGGTAC

Contig 5 (1730 bp)

CGTACCCCGCAGAGCCAGGCCCTTGGCTCAGCCCTCCACCCAGGCCACGTTCCGCCCCCTTCTG
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 CTGCTTACGCCCTGGATGACACCTGGCTGAGCGGTGGTCCCGTGTCTGAGGGCAGCCCCACACAGCT
 CTGCTCACTTGGCTTGTGTCTGTCTCGCATCCGCTCATCACATGCCATGTCTGGGGCAGCGTAGCGCTTGC
 CTTGTGTGGCACTGTGGCACTGTCTCTGATGGGAAGACTGAGGCTGGGGTCAAGGCCCGCTGTGCCACCC
 TCTAAGGACATTTGCCGGTGCAGCTGCCCTCAGG
 CTGGCCCCCGGATTGCATCTGCTTCTGGCAGGATGAAGTGGCACCTCTGCTGACCATTAGGGCTGTATTT
 GCCTTCTCTGTGGCAGTAAATATTACTGTCTCTCCCTGTCTCTCCAGGCCGAGNCCAGTCTCTCAGGGGC
 ATGGGAGGTGGACAAAGGTGCCAAGCAGCCCTGCTCTTGGGGGCCAGTGTCTGGTGGGGGGCTGGGCT
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 GGTGCCAGTGTCTCACTGGGTGGGCACCTGTCCCC
 ACCAGGCAAGGTGGTCCGAGCGGTCTTACAGACAGAACCAGCAGAGGGCGCCAAAGCCCCACTTTTGACAA
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 GTTAGGAGGGAACAGAGGGGACTCTGGGGGTGACTTCTTACGCGCCACATTCGGGCCAGCAAAACCGAGG
 CTGGAGGAGGCCGGGCACCTGTGCCAGCTGGAGCTTGTCTGAGGGTCTCAAGGCTGGGAAATTAGGGC
 TGGGGGTGGGGGTGTCACTGTCTGGGCCAGGAGG
 CCCCCTCGCTCTGATTGGAGCCGCTCGGCCACTTGAGCCAGGAGGCTCACATGAGGCGGGGGCTGCAGGGACA
 GGACCTCGGGGCCCGGAGGGCTTGGAGGGGTCCAGCTGGGCCAGGGTTCGTTCTTCCCGGGTCCATGTC
 CACCGCCCTCCGCTGTCTGGAGGAGAGGAGTCCAGGGCAGAAAGAAATGCGTGGGATGGGGGGGTGGTCAG
 GGGTCTGGGAGCTGTGAAACAACAACAGACAGCGAGGTCTGGGGCGCCCGGCCCGCCCTCCGCA
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 CGGGTCTCAGCTACCCCTGAGCTAGCCCGCC
 ACTCGGCTCCAACCTCCCGCAGGGCCCTGGCACGGTCTCCAGGAGTCCACTGAGGGTCCCCAAAGCTGCCAC
 CAGGAGCTGGGCTGGGTCTGTACCAACCCACCCACCTCCAAGTCTGAGATATG

Contig 6 (4833 bp)

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 GGGACACACCTTGGCTCTCAGGGTGGCCGTACAGAGGCGGCTGGGTCTGANGAGGTGGGGGGCTCTGGGG
 ACCGCTGGTGTGAGTTCAGGACGGGGGTGATGCCACCTCTCTCTGAAGGTTTGGTGGGTGGGGCTTCTCTAT
 CGTGATGACAATACTGATTTCTGGAAGAGCCAGGTGTTTTCTGAGGCTGTGGTGTGCACTTCTCCACGTGGCCA
 CAAGGTGCCGGGCTGGGTGAGATTTGAAAGCCCTCGGGAGCGGGTGTGATGCGCAGATTACGCTGTGCT

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FIGURE 6, CONTD.

CCTCGGGGTCTGGGGTCAGGACGTGGTCCCCAGCAGTCTGCTCCAGAGCCTGTCAGTGATGTGTGGGATTTTA
CCGCTAGAACACAGTTTCTCTGATTCTCAGAAACAGCAGATGCTTTAGGAGGGGCGTCAGGTTTACCTG
TGCTGCANNGCCCCCTGCCACCTGGTCCGAGCCNCAAGACGGCATCTAAAGATCAGTTCTCATCATCAGTTC
CGCAGTGTGGGGTGGGGCAGATGAGAACCTCAGGGCTGGGCGCAGAGGTGGGAGCCCGCTGGACCCCGA
CACTGCAGGGGGGCCCTCCCCCTGTAGGAAGAACAATGTCGCTTTGCCACCCAGCCCTCTCCCCAGGGTGGCC
CGAAGCTTTGCTCCTAAGACCTCTGGGCTGTGTGCTGTAATTCATATAGTGGCCACCAGGTGTCAGCAGGAGG
CCACTTAAGCATCCATGTGGCGGAAACCTGGAGCTGGGGTTCTAAGGGTCCCTCGAGTGTCTCTGAATAA
ATAGGCGCTGACCTGATCCCCAGGAAGGGATAACCCCTCTCCAGGCCCTAAGAGGCAGTGGGCAATGAGGTTT
ATGTGTCCACTGTACCCCAAATTTGCTCTCTCTCCCTTACCTGTGTCCCCACCCTGGACGATACACGGA
GTGCGAGGCTGGGGTCACAGCCCTCACAGCCCCAAAGCTGCAGGTCTGCTCAGGGGACCCGAGCTTGGC
TGGTCCCCCTTGGGTCTCCCCACCTGACCCGCTCTGCTCCCTCCCTTTGCTTAATGCTCTGCGTTTC
AAGTTTGTATGGAATAAATACCCCTGCAGTGGTGTGTTCTCTTTGGGGCTGTGCCAGAAGTGGGATTC
GACCAGGGCAGAGCTCAGATTCCACATACTGTGTTAGGGATGGCAGGTGCCACATTTCAGGAGTTTCATTGG
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GTAGGGGCGACAGGCGGTGAACACTTGAAGCTGCAGAGCCAGAGCAGAGCCAGGAGCAAGTACATGCTC
CCCCACCCAAAGAACTGTGGGTGCGTCAACACTCCCCACTGTGTGCCCTGGACCTGACAGGGCCTTTAGCCT
CCCTGTCAATCTCCCAACCAAGAACCCAGTGAGGCACCCACTTGGCCCTCTTAGTGTGTTATGCTATGCTG
GGGATCTGCATTTGTTTAGGACACCCAGCTAGATTTAAGTCCCCCAAGTGTGACTTTTCTCTCCACTG
AAAACCTGTCTCCCAACAAAGGGCCCTATCCCTTTAGCTGAGCCAAAGGAAATTCAGGAGGGGCTTGAATG
ACAAAGGAAGAGGGGAGAGTTAAACCCCAACACTGGCTGGCAAGCTGGGTGGGGTGGACACCCAGGGTGA
GGGGTGCAGTGAAGGTAGCGGCTGGTGGCCCTTCTGGAACACTACATGTGACTTTGCCATTAGGTGAGTCTTTGC
TTTGGCCCTGCTCTATCTCAGGCTTATGGAAGAAGTTAAATTCAGGAGCACTTGGTCTAACCCAGGCAAGC
GCTTGTATCTGGGCCCTTCCCCAGCTGCTGACCACCTGAGTCTGCGCCTTAGTTGGAGTTTGGCCAAGCTC
AAGAGGCTGTGGACCCAGTCACTCCACCCAGGGGTGCTGTGGGACAGGCTGCTGCTGCCATTTGCTGTC
AGTATGTCACCTGTCCGGCACACACATGCTGAGGGGGTGTATCAGGTGCCACTGGGGAAGGAGGAGAA
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CAGTTGCCCCAGCAGCCCAAGCACTAAGTTGGCACAAGCTACCCAAATTTGAGGGGGCTTGGGGAAGGG
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CAGCTTTGTCCCCCTCTCTCTCAGCGGCAACCCGGCTGGAGGGTCTGGCCACTACAGCCAGAGCGCCCC
TACTTTGGTGGCACTGCTACTATTGGCCCAACACCGGATCACCGCCAGGCAAGTTTCGGCAGAGAGTCTGG
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CCGAGGCCACAGAGGCTTTTGAAGGAAATAGGTTTCCCTCACTAATGCAGCAGGCAAAATGGGAGGGGCA
GGGGTGGAGGGTGTGCCCCCCCCCCAGCAGGAGGGCACAGCTGTTTCTGCAAAATGTAAGAAAGCAGGGTTT
TTCTGTGTGAGAAGTTCCCTTTGCTGCTATGTCACCCCGCCCAAGACAAACAGGACACTGTGCAGA
GGGGCAGAGCCCCGAGATTTGGAGTTGTTTTATATGCATATATACCATTTTGAAGCAAGCTTCCCTCT
CCCCACTCCCTACATGTCCCCCTTCAACAAAAATCCACCAGCTAAGTGAAGGGGAGTGAGAAGGACGA
CGAAGGGGCACTGTCCCCCTCCGCTCCACAGCGGACTTAAACGTACAGCTTTTCGCTCCGGACAGTGTGC
CGCCCCCTGGCCCCCTCAGCTCCCTGCGCGGGGGCTGAGTGTGGGGCCAGGGCCTGTCTCCAGGCACTGC
ATTATTTGTGCTGAAGGTTTGTCCCGCCACCCAGGCTGGTGTGGGGGGAAGGGTTCAATGCTCCAAA
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GCCCTCTCTTCTTATTTCAAGGTGAAGTGTGGGGGAGGAGAAGGTTTATATTGTGTCTGTGATC
CCCCAGGACAGGGCATTTGTGTGCGGCCCCAGCCCCAGGCCAGGAGATGGGCCAGCCTGCCGACAGA
AGGGTCTCTGCTGCTTGGCTGCAGGGAACCCAGCTCTGGGTGAACCGTGGGCACCTTCTCTCTCATGCC
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GACCTGCGGGCTCTCCACCCAAAGAGTCGGGGTGGGGGGCGGATTTGGTTTGAAGAGAAACAATAGGAAC
ACACTCTTTATTTTCCCAAGGGGCCAAGAGTCAACCTGAACTTGAAGACAGGACCGGATTCAGCCCCC
AGCCCCAGGGCCCCACATCTCTCGGGCTCAGCCGGCGCCCCAGCTGCCCCCCAGCCTGAGCTGCAGAGGC
CAGGGCTGCCCGAGACCCAGCCCCAGGTGAGCTGCTGCAACCTCTGGGCCAGGAGATCTCCGCGGGCTCAG
AACTGAGGGCGGGCAGCCCCACCCAGCCACAGCGGTGAGTGTCTCCAGACCCAGGGCAGGGCCCCGGTGTCCC
CGGCACAGAGAGCTGTGCTGAGGCCAGACCTCCAGGCGGTTTATGTTCCCATCTCCCTTGGGGAGGGG
TGGGCTCAGAGGGGCTGGGGTGCATCCGAGAGCTGGGGTGCAGGGCTCCAGGTGCTCTCTCCAGGCGGC
TGGCCCGAGGGGGG

Contig 7 (2014 bp)

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FIGURE 6, CONTD.

CTGGTTTCGCACTCCTCCGGGGACTGTTGAAGTACCGAGAGCGCNCGCGGAGCGCCGGGGGAGCGGGGGTG
GCCGCCGGGGGTGCTCCCGGGCCCCGGACCGAGCCAGGGACGAGCCTGCCCGCGCGGCAGCGGGCCGCGG
CTTCGCCCTAGGCTACAGCGCGGGAGCGCTGGGGCGCGGCCGTGCCGGGAGTCCGCTGCTCCTCGGAGG
CGGCCGACCGGGGAGCCTGGGGGACCCCGAGCGCCCGGGGAGCAGCGCCCGACACGCGCCGGGCGCTCTCG
GCTTCTTCCCTTCCAGCGCGCGCCCGCGCGGGCTTCGGCACCGGGGCGCTCTCAGTGGCAGGAGAAGCG
TGCGCTCCCGCGGGGTGGGGGACCCGAGGAAACC
CGCACCGCTGGAGCGCGCGCGCGCGCGGCGCAGCGCTCGCGTCCCCGGGGAGGGCGCCACTGCTCCGCGCGG
CGTCCCCCGACGCGCCCGCGCTTCCCGCGCGCGCGGGATCCTAACCTCTCTCTCGGTCCGACGCCCGCAT
CCCCAGGGCTCCAGGCGCCCGCGCACTTCCCGCTCTCTCCCAATTGCAGACAGCACTTTTCTGGGACCTCCC
AAAGGACAGCCTGGCTCCAGGGTCCCCAGATACATTACCAATTTCTCAGATCACAAGTGGGTTTTTCGGGC
ACTAATTCAGAGACCTCAAAGCACATGAGCCCTACTGGCTTCCAGGTTTCCACTAGTGGCTCGGTCC
CCACTCACTGGGGATTGTCTCCAGGCTCTCGC
GGTGTGATCCCACTTTCGCGCCAGGTCCCGCAGTGCCAAATCCCTCTCTAGAAAACTTAAACACTGACTC
CTGGCTCGGGGTGAGGCTGCCAATGTGCTGACTCCCGAGAAGGTATACAGTGTTTTTCTGGCATTGGG
CTGCTTCCCCCAAAACAGTGAAGCTCTTTTCCCGCTCCCATAAATTTGGACGCCAGGGGACCCCAAGCT
TAGCGCCCTGTGTTGGCTCCCGCACCGCGAAGCCCTGCTCCTGGGGTTTACGACAGTTTGGGACTTTATC
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CCCACTCCAGTACAGGAAGCGATGCCCCAGGGA
CCCTCGGAGTTGGAACTGGGTCTCTTAAGCTTCAACAAATTTAGGGCTTTCGCGCATGGCGCGCTGATGCC
CTTGTGTAATCAGAACTCTGCGCTCTGATTCTCTGCTTCCACAACTTGAAGCATGATTCTGTGTCGCC
CAAACTCACTGAGCAAAATCTTTTGTGGGGGCTGCAAGATAGGAGGCACTTCTCTCCGAGCTCTCCAAA
CTCCCTTGCTATAATCAAGTTCCCTAAACTTAGACAGAGCTTCCAGGCCCGAGAGGCACACAGAGCCATT
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CCTTGCTCCAGCCAGCCCAAGCAAACTCTTGC
ACAGATCCCATATCTTGTGTTATGTCAAGCGCTTTCGCTGCCAGTAAACAAATAGTCTGAGTGTCTTCTCCAC
CTCATAACTTCGGAATATTAATAAATTTCCCTGGGCCCCCGAGCTGACAGACAAAGATCCGGGCTCTCTAAA
ATTGAGAACTGATTCCAAATCCAGGCCAACGCCAGACCTCTCCCAATCTGGAGCCCTCCGACTGGACAC
ACTGAGCTCTTAAGTATTACGCGCTGTCTCCAGGCCACCCAAATGCATTCAAAGTGAGCCTTTGGTACAGA
AAGGCACTGATTCTTGGGCTCCAAAGCAGCCCATGCACCCCGAGTCAACCCAACTTAGTCAGCACTTCCG
GGGTCTCCCTCCGCACTGCAAACTCCCAACTGCGG
ACACCGGTCTTTCAGGACCCACCGCTAGACGGTCTTAATCCCTTTTCCCCAGACCTAGATT
Contig 8 (371 bp)
AGATTCAAAACTATTTTTCTGGGCTCCAAATGAGGTGCTGCCAGTCTCCAAATAAAGTGGG
GTTTTTGTGTTGTTGTTTTTGTGTTGTTTTTTTACCTTCCAGGAAACAACTCAACTTTTTGGA
CCATTGATTATGGGTCCCTGACTTATGACCTTGCCCAAGTCCCTTAAATGTAGGCCATTTCACGG
CGCTCCCAAAATGAAATGCCCAGATCCCGCGGAAAAAATATCCCGGGTCTGGAATCCAGGTATTACA
GGCTCGGCTGACACCCCTCTTGTACTAACAGGTTCCTGAAGTTTAGAGATCACTACCTAATGAACA
ATCCAC
Contig 9 (2415 bp)
CCAAACTGGGGCCCTATCTTACTAGGTTCCCTAAATGCAGACAGCGCCCGGAAAAATAGGGCGTTTTTT
TCCTGTTTCCCAAAATAAATAATTTGAACCAATTTTAGAATTAATAATGACCTTGATTTTCTGCT
GTTTCCAAATGACTTTTACAGCCAGGTTGCCCGAGTTTAGACGGTGTGCTTGAATCTCTAAAGCAC
CTGAGGATTTTCCCGAGGAGCCACCACTACCGAATTTACTGTCTTCCGGGCGCAAGCCTCCAGGCC
ACCAACTTGATTTCTAAACCGTGGAAATCAGCTCCACTTCCCTCCGCGACCCCGAGGGTCTGCTCAGACCC
CCCAACGTGCCCGCTGTTCTTCTCCCGCAATTT
TTATTTAGAGAAATGCTCTCTCGGGTCTGCCAAGTTTCCCGCTGAGACTTCTCGGTCTATCCCAATCC
TCTTCCCGACAGTCCGGGAGCCCCACAAGCTTACCGACCCACATGCTGGGTCCCGCACTTAAACGCGATC
CCTGTCCCGCAGATTACCCGAGTGATTTCCTGCTCTCAGACTGGGACTCTTTACTGGAGTCTCGAATTT
AGCCATTATACAGTTCTCCACTCCGACGAGGCTCCCTTGGGTCCCGACGTCGGGGACATGGGTCTCTTG
CCTGCAAAATCAGGCTGCTGACTTGACTTCAAGGCTTTGGGCATTGTTCCCGCGCCCGCGGGTCTCGGTTC
TCCCGCATCCCGCGCACGAGGGCACTGGGTCTG
GGCTCTTGGGTGCTCTTACAAGTCCCGGAGCTCCTCGGACTTGGGAAGTGTCTTTCGCTTCCCAATAC
ACTCGGCGCGGAGTGCTCCGCGAGGAGTAGGACAGCTTCTCCCGCTCCAGGAAAAAGCACTGGGCATTG
CCCCAGTTTCCCGCAAAATTTGGGCATTGCTCTGGGTCTTCAACGAGTGGGCGTTCGCCCGGACATGC
GGACTGCCCGGGGCTGCTGCTCACTTCAAGCGCTCCACCGCCGCTGCAGAGCGCTCGCTCTCGCTCTC
GGTCCCGCGCGCTTGGGACGAGCTCCGGGCTCCAGCTTCCGCTGAGCTCCCGCTGCGCTCGGCTG
CCCGCGCGGCTCCCAAACTCACTCGCGCGCTC
CGCTGGGGTGGCACTGGCTCCGCGACTGCGGGGACAGGGAGCGGAGCGGGAGCGCTGCTCAGGCCA
GCCGCTCGGCGGGCGCGCGCTGAACGCGCGGCTTCTGTTGCTCTTGAAGGTCAACCGTGG
GGAAACGCTCGGCGCGCCCAAGCGGGGAGGAGGGCTTGGGAAGGAGGACCGGGAGAGGAGCAC
CCCGCTGGGGCGGCGAGCGCGGCTCCAGCGCGGGGAGGATCCCGGAGGCGCGCGGAGCGCGG
CGGAAGTGATTGATGGCGGAGCGAGGGGGGAGCGGATCGGGGCTTCCGCGCGCGCGGGCCCTTCCCTCG
GAGGACTCGGGCGGCGGGTTCGCGGGCGG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

CGGGGCGGGGGCTTGTGCGTGGTCTCCACTTGGTAAAAATACAACGACTTTTACGTGCGCCCGACTCTC
CAGGAGATGGTTTCCCGAGACCCCAATTATCGTGGTGGCCCCGGGGCTGAACCCGCGTCTACGCAAGGCC
AACGCGCTGAGGACGGGGGAACATTATCCGGATATTTGGGTGGGCCCCAAAGCGAGCTGCTTAGACGCGC
CCCGGTGAGCTCGGTCTCGAGGTAGGCTTGGAGCGAGGTTCGCCGCCCTGCTCTCTCTTCCGGCAGGCG
CGGCGAGGCGGGCGGCCCTCCCCACGTACGGCACCTGGCGGCCCGGAGACGACTCCCGGTTCGCCGCGG
CACCGGGGGCGCTCGGGCTCTGGCTGGGCTCGA
GGCGCTGGCGCTGCTCGGGCAGGTGGAGGCTTACGCCGGGGCGGCGCCAGGGACGACCCCTTACCCGCGAG
GTCCCGAGCGGACTCGGGGCCCCGGATCCAGCGTCTAGCCACCTGTGCCCGCACCCGCGGAGGGCTTGTGA
CACCTACCACCTGGCGGCCCGCGTCCCCCGCGCACGAATGTAGGGATCTGACACCCCGGAACCTAAGAC
GGGGCCCCATACACTTTCGTACAGCGATTCCGGATTCTCTCGAACTCTGCGATCTGTATGGCAAAAGTTGA
TGGCTGCAATTATTTTCTGATAATTCAGCGAAAGATGGCGACCAGAGCTATGCGCGTCTGGGTTTAAAGGC
GAAACCCAAATTACGATCTGGTCAACGAACAGAT
ACAGCATACGTTTTT
Contig 10 (3753 bp)
AGATTCCAAATGGGATCCCGATCAGGAACCCGCTGCTCGTCTGCTCGTCTTCTTGCCCTTGGCCCTGCTGCTG
CTATGCTGCTTACCGCCCCAGTGAAGTCTGTGCGGCGGGGAGCTGGTGGACACCCCTCCAGTTTGTCTGCGGG
GACCGCGGCTTCTACTTACGTAACTAGCTCAGCGGGGACGCGGGGCGGGCGGACACAGCAGGTGCTCCATCG
GTGCTGCCCGGCTACCTGTGCGGGTCTTCCGGATGGATGGTGTGGGGGACGGGGGCGGGGGGCGGCCAAGG
GAGGAACCTCTCTCCGAGGGTCTGAGACTTACAGAGCGGGGGCGCCCTGGCCCTGCGCAGTGATTGGCACTGC
CATGTGCTTGGCTGGGCTCACACCCCTGACGTTCTTGCAGCGTGACTCGAAACGGGAAACCGAAGGGACGG
GTGGCACGGGGTGGGAGGGCAGACCGTGAAGTGGCAGGCGTGCAGGGGTTCTTTCGGGCGGGGTGGCCACGCG
AGGCGCGAGACCTTCCGCTCCCGCTCTGCTGTGCGCAGGAGCAGGGTGGACCCCTCCCTTGGGCTCTTGGCTG
ACATTACCCCATGGTATTGTGGTGGCTGACGCTTGGCAGTGGGCGATGGGTTCATGGAAGTGTGGATTGAAG
TGGATAGATGGGTGAAAACCAATAAGAAATAAGGCCGCTGTGGCTGGCGGCATCTGCGAGAGGTGACCGC
TGCCCTCCCTGGGCTTGGGCTTGGGTGGGTTCCTATGGGTGGGGCGGGCGCCATGCAAGGTGCGCGCTGCTG
TGGCTCAGAGTCTTGGCGTCTCATCTTCTCTGCGCCCGTCCCGCTCTGAGGCTGGTGGCTGGG
CCCCCGGAGACCTTCCGCTCCCGCTCTGCTGTGCGCAGGAGCAGGGTGGACCCCTCCCTTGGGCTCTTGGCTG
CACCTCCCGCAGGCTGGGCTCAGTGTCTTACCTGTAGGATGGGTGAGGGGCTCTGAGAGAGTCTCTG
GGCAATAGATGGGTGAAAACCAATAAGAAATAAGGCCGCTGTGGCTGGCGGCATCTGCGAGAGGTGACCGC
CAGCGCGCTTGGGCGGGGAGGGGTGGGGACGCTGGCTGGGGCAAGTTCTCAAGGGCGCGAGGCTCACCC
CCGCGCATGCTCCCCATGTGGCAGGCTCTTCTGCGGCTCTACTTACCCACCCCTGAAATGGGTGAAAC
ACCCATCTTGGCATGCAAGCTTCTCTGTAAGAAAGCGTTGCTGCTCTTGTATGCTCTGAGGCCCCCTGCTG
CCCTGGGCTCTGAGCCCTCTCTCTCTGCTCGTTTGGGGGCGAGGAGTGGCACCATAGAATCTGGGCTGGG
CCTGGGAGCGGCGCCCTCTGTGCGAGGCTTCCCGAAAGGAGGGTGGGCTGAGCTCCCGACCCCTCTGAGCC
CTTACAGGACCCCTTACAGGGGCTTCCCCCCCCCCCCCGGTGGCGGGCGGCTGGGCTGGGCGCTTTT
CCTTGCAGCCGAGTGGAGCTGTGCGAGCGGAGGGCGAGGACGGGAAGAGAGAGGGCGTGGTTTCTGCTGGT
CCTCACTCTCTCTCCCGTCTTCTCTCTCTCTTCCCATTCCCACTGTGCTTCCGGGTCCCGGGCGCGAG
GCTGCCAGGCGCTCTGATCCATTGGGGACCGCACTCGGGTCCCGCTGGGCTTCCGGTACGGGCGACGGC
CCACCTATTTTCAAAACAGCCTTGGGTGCGAGGCCAAGAGGCTGGGCGCGTTTAAAGACGGGAGGAGGCG
CAAAGAGGCGAGGGCTGGTCCCGAGCAGCGCCGACCGCTACCCCGCTGTCCCTCTCTCTTCCCGGGG
GGCCCTGTGCACCCACTCTCACTTCTCTGCTCGAGGCGACGAGGCTGGCTGTCCCGCAAGGTGACCGGG
CGTCTGTCTGGAGGGCGGGGCGGGGCGGCTGGGGCACCGTCCGTGCGCGGGGCGCTGTGCTGACGTGC
CTTCCCTTGGTCTGTGGGACTTCCAGGCGAGGCGGCAAGCGCGTGAACCGCGCGAGCGGTGGCATCGTGG
AAGAGTGTCTTCCGTAGCTGCGACTTGGCCCTGCTGGAGACTTACTGGCCACCCCGCGCAAGTCCGAGAG
GGAGCTGTGACCCCTCCGACCGTGTTCGGTAAGGCGAGCCCTCTCTCGGCGAGCGCCCCCCCCGGGGGG
GGCTGTCTCTCTGAGCGGGGGACCGGGCGCAGCGGCTCTTGGGCTCAAGTGTGCGAGAGGGGCTTCT
CCCGTGGGACCTTGGCCAGAAGCCAGGGCAGTCTTCCCTCTGTGCGAGGCGAGGCGAGGAGGACCCCG
CAGAGGTGTGTCTTGGGACAGGGGCTGGGGGGCAGGCCCCCCCCCTGAGCGGCGCTTCCCTCTCAGGACA
ACTTCCCCAGATACCCGCTGGGCAAGTTCTTCCGCTATGACACTTGAAGCAGTCCGCGCAAGCGCTCGGAG
GGGCTTCCCGGCTCTCTGCGGCGCCCGCGGGTGGCAGGCTCGCCAAAGGAGCTGGAGGCGGTGAGAGGCGC
AAGCGTACCGAGCCCTGACCGCGCTCCACCCCGAGACCCCGCGCCACGGGGCGCTCTCCGAGGCGT
CCGGCCATCGGAAGTGAGCCAAATTGTCTAATTCTGCGGTGCCACCATCCACCTCTGTGACCTCTCTCGACC
GGGACCGCTTCCATCAGGTCCCGCTTCTGAGATCTCTGTACCTTCTGTCTGCGGGCATCTCCGCGCGGGC
CCGTGCGCCCAACCTCCCATGTGAGGCTAGTCTCTCTCGGCCCTTCCATCGGGCGAGGGCATCCAAACCA
CAAACCCAAATTGGCTTGGTCTGTATCTCCCCCAAATTATGCCCCAAATTATCCCAAGTTACATACCAAAAA
TTGAACCCCTCAACACACCCACATACATCAGCCCCGTAAGCAAGTTGGCATCTTAAACACCCAGAAAA
GCGAATTAGCTTTAAAAAATAAACCATAATCAATTAGCTGAAAAAATA : TACTAAAAATAAATTG
GCTTAAAAAATAATGGCAAAATAAAGAAATTGGCCCCCGCTTCTTCTTCTTTCGGACCTTGAATTGA
AATTGGCTGTGACCATCATCAAGAGAAAGGAAGGACCAAAATTGAGGTAGGCTTGTGCGCGCTCACAG
CCATCTCCCTCTCTGCGCACCCCTCGCGGCCACTGGCGGTGTGGCACCAGGACCCAGTCCCGTCTCTC
TCTAGTCCCATGACCGAGACCGCGGTGGAGTGGCTGGGAGACCCGCTGAGATCAGAGGAGGGGAGCAGGAA
CCAGAAACCCAAACCTGCACAGGTACAACATGACTGGCCCCCGCACAGCCCAAGACCTCTCATCTCAGTCTC
CACTTAAAAAGCACCTGTACCCACAGCATCCCTGCAGAAACACACACACACACACACACACACGCGACGCA
CGCACACACGCGCACGCGCACGCGCACACACTCATGCTATACACACACACACGCGACGCGCAC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

CCACACACACATGCATTACACACACACACTCGTGCATACACAGTGGCGCGCACACACACACACA
CACACTCTCTCTCTCTGTGGGATCCCTGAG
Contig 19 (500 bp)
TGGCTCTGGCATAGGCTGGCAGCTGCAGCTCTGACTGGACCCCTTGCCCTG
GGAACTCCATATGCCGTGGAAGCGGCCCTAGAAAAGCGGAAAAA
AAAAAAAAAAAAACAACCAACAAACAAACAAAGCCAAACACACAGAACTC
ACAGACACAAGAGAGACTGGTGGTTGCCAAAGGTGGGGTCGAGGGTGGG
AAAAATGAGGAGAGGGGGCAAAACACACAAACGTGCAGCCATAAAATGGT
AAAGTCCCGGGGACCTCGGTAGCGCTGTGGGACTCGGGTTGAGAAC
CACCCTGATGTGATTCCGAGTTGCTAAGAGTCCCTGTTGGAGAAACAA
ATGCGTATCGACGTGTGGAATGAAAGTTAACCCGACCTGCTGCTGTGAT
CACTTTGCAACACATACAGACATAGAATCATTATGTTTACCCCTGGAGC
TGACAGCGTTATACGTCCCCAGCCTCAATTTAAAAACAGCGTTGCCGTG
Contig 20 (400 bp)
TTCATACCTGTGCAATGCCAGCCTTAAATGCACAGAGGAGAGCATTAACTT
TTTGCAGAACTCACTGAAATGATACCACTCATGTTTTCGAACCTTGCACTT
GGGCGTTATTTTATTTGGTGGCGGAACAGCGCGGATGGACCAAACTAG
CGCCGCTGTTTTTATTTCCCTCGGTATCGCGCTCTCGCTGCTTCCCTC
CCCTTCGCTTGACGCTGAGGAAAGGGCTGAGAGGAGGAAAGTCTGCATT
CACCATCTCCCCCTGCCTCTGTTGTCTATCCTTCACAGAAGTGGTGGCCT
GTGGGGGAAGTCACTAAACCTAGGCAGGTGTCCCGTGGGGTCTGCTTG
TTACACCTTTGTGCACTGGCCCAAGTTCTGGGTGGAGCGAGAACGTGGC
Contig 21 (559 bp)
AGCTAGCCCCCAGCCAGGGCCAGGCTCTCTGCCACCCGCCAGCCA
GCATGTCTCAAGAGGAGGGGGCTCTAAGGGATGAGGACCTGCTCCAGTC
GGAGACACGAAGCCCCCGGCTCTCCCGAAAGTCCAGCTGCGGCTTT
CGAGCACGGCTGCGCCCTTCGTCAATCATTTAGCCACAGAAGTGAAGG
CGCTTTCTGTGGCCGAGGCAGGCGGGACACAGAATGGAATCCACCCAGA
GCGAAGAGCCGCGCTGGGTGAAGCGGCTCTGTGGTGGGACCGGGCGGG
AACTTCACATGGGGTGGCTGTCCCATCTCCCATCTGCTATTACTGCAG
GGGCTCGGCCACACCCGAGCTGCGGGGGCAGTGTGGACACTGGACCT
GGCTCCGCTCTATGATGTCTATGGGGGGGGGACAGCAGGGGAGTGGC
CACACCTCGGGCTCCAGCACAGCCAGGATGCGAGAGGGCCCCACCC
ACCAGGGGCATGTACATCCAGAGGACAGCTGAGCAAGCTTGATANG
GGCTTCAAC
Contig 22 (450 bp)
CGTGAGGGGACCCGTGCGGGCTTCCTGTGGCCACAGAGAACAACACAC
CATATCTTCAGCCCCACCGCGCGGCTTTAATGGGTAACTGGGGCAA
GGGGGCCCTGCTGAGGCGGGGTGGGAGCGCAAGGCATGGCTGTGT
GCCCCAGCCAGTCTTCAGGGCGCTGCTGCTGACCCGGGGGCCCCAG
GAAGCAGAGCACCCAGCTTCTCCCTATTCTAGAACCAGCCCCAGAAC
CTGGACCAGACCCAGGCCAGGGGATCTGACAGAGCCAGCGCAAGCGG
GCCACTCCACACCCACAGAGGGGGCAGCAACCCAGTCACTGCGCAGC
CCATGCCAGGGGGCAGATGGGACACGAGAGCAGCCCTCATCCACAGCAG
GCAGGGGAGTGAACGTGGTCAAAACGGGGCGGTTCCACGAAAGTTAAGCA
Contig 23 (535 bp)
TGCCAGAGACCTCAGAGCTGGGCTCTGCCTTCCCGGGCTGACACGGAGGG
CTGTGGCTTCCACCACCCAGGCCACAGCCAGCCTGCCAAGTCCCTGAA
GTGTCCCAGAGGTGGCCCTGCCTCCACGCCAACATCAGGCTGTGCA
GCCCCTGGACGGCCCCCTGTCCCCGGAAGCCCTCGGGCTCTCTCGGCTC
GCCTCTGGGGAACCTCGGTAAATGTGGCCAGCCGTGCAAGTGGCCGGATC
ATTTGCTCAGGGGGGCCAAGGCAGGGGGTGACACATCCGCAAGTACCG
CATATGCACAGGATATGGATTGGGTGTGGATTAACTTTTCGCAATGT
CTCTGCCGTACAAATATTGTTTCTAATCTCTGCCTCCCTGAGCCGGTG
AGTCTGCCCGGAGCTGCGGGGAGCTGGCTGTCTGAACCTGCCCTGGCCC
CCACCCCCAAGGAGCCCCCGGCCAGTGTGAGGGCAGGAAGCTTGGGCA
CAGGCTGCAGAGGCCAGCGCTGGCTCAGTACCT
Contig 24 (868 bp)
TATTGAAGACCTATCATGAGTTCCAGAGCGAGGGGTGGAAGCAGGGG
CCTACAGCCCACTCCCATCACTCCAGACCCGTCCGGGCTGGTGTCCC
TGCCCCCTACTCTGTCTGTGGTGGCGGACGCTCGAAGGAGGCACTGTG
GCCTGGAGCCTGGAGGGTCCCTGAACCTCCCGCTGCCACTGGGCCCTCGG
GCTCTCTGCGCTGGGACCCGCGGTGGTGGGAAGCAGCCCTGCTCAGTG
GGAGGAGCAGGGCTGTGGCGCCCGGCACGGCCCTGGGGGGGACGCACG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

CAGGACGCANGTGGGCGTGTGTAGTCCGTCTACACGTCCAGCCAAGGGC
GGCCGCGACCGGCCAGGGTGGGCAGCCCCAGCCTCAGCAGGGCGCTCTCT
GGGGCTCAGGCTGCCGCCAGGGAGATGAGGGGTGAGGCGCAGTCTGGGG
CTGCTGCCGCGAGAACCCTGCCACGTGGCAGCTGGGCACAGGGAGACCTG
TACTCCAGAACCTGAGGCTGGACGTCCGAGACCCGCGTCCCGGCTCTT
GGGTGCTTGGTCAGGGTCTCTTTCTGGTTTGTGGGCAGAACCTCTCTAG
CGCGTCTTGCATGGGGTGCTAATCACGGAGTAAGGAGCCAGAGAATGAG
GCACGGAGTATCCAGTGTAAACCTGGAGTATGGAGACGGGAGTACTAAT
TGTGGAGCATGGCTCTAAGGAATGGAGTATTCGTACGGAGAACGCGGGG
CCGGGTGAAATACGGAGAGCGCGGTACGGACAACGGGACGGGGTATCCG
AAGGGGAGGATGGAGTATCGGCCGAGGGGTGGAGAATGGACACTAGAGGA
TGTATANNNGGCGTCAAT

Contig 25 (500 bp)

ACCAGTTTCGATGAGCAATCCCAGCGGCGTAACATTATGGGTGCAGCCTG
GTCAATGCGGGTGGAGTTTGAACCTCCACGCGTGGCGATTGTGGTAGATA
AATCGACATGGACAGGGAGTTGATTGAACATAACGGTAAATTTGGCATC
CTTTACCGGGCGTTGCAGCAACTAAGTGAAGTGGCGGTGGGAAGTGT
GTCCGGGCGTGATGAAGATAAATTTAATTGCTATGGCATTCCGGTTGTGA
GAGGCCCGGTATTGGTTTGCTCTGGTTCGAGGAAAATGCTTGGCGTGG
ATGGAGTGTGATTGCTACCTGCGACTTCTGCGCAAGAAGAAACGACAC
GCTGTTTGGCGAAGTAGTATCAGCAGCGGCGAGACGCGGGTATTGTGCG
AAGGCCGCTGGCAGTTTGTATGATGATAAGCTCAATACGTTGCATCATTTA
GGTGTGGGACGTTTGTACCAGCGGCAAGCGTGTACGGCGGGTTAAGC

Contig 26 (900 bp)

ATGTTTGTATGTCCGCGGTGCTGTAAAAATTTACGCTGCTCGCGTTCTTT
GGCTTCGTCCACCCAGCGAAACGGACAAATAATTTCCGTCATACCTTTT
CTTTACGGCGGAAGCCAATGTCGTAATCTTCAGTAAGACTCTGCACGTGCG
AAAGCAATACCGTCACCGTCAGCTAACAGTGCCTGACGCGCGGGCGGT
GAAACAGGTGCCGACGCTGCGCTGGGCACTTGTCCGGCGAGGGCTTAC
GCACCGGAACATCTTTGCCATGCAGCTCTGAAAACATCAATGTAAGTC
ATGCTGGTGAAGTGCCTCATTTGCGTTTGAACGGATACACCGGGATCTG
AATCAGATCTTTACGCTCGACAGATAGTTGAACAGACGCAATTCATCG
GTGAAATCACATCTTCCGCGCTATGCAGAAATAAACGAGCAAAAGCGAAA
TTGGCGCTACGCTCAAATGGGTGATGGCGTCCAGCACGTTGTTACAGACA
GTCGGCTTTGCTGGTGGGGCCAGGACGCGCGCAGACTACCTTATGCACAT
TCGGGAAGCGAGCGCACACTTCGTCAACATCAGCGTGAGTATCGGGGTGCG
TTGGGGTAGGTGCCAACAAAGATATGATAGTTTTCGTAGTCGAGCGTGGT
CGCCGCCAGCTCGGCCATATTGCCGATGACGCCCGTTTCATTCCACGCGG
GAACCATAAATCGCTAACGGTTTTCATCTGGTTTATACAGTTCCGGGTAA
CTCATTCGCGGGTAGCGGCGATAAACACTCAACTTGCCTTTAATGCGGCG
TACCCAGTATACGACATCTATAAAAAAATCGTCCAGCCCGCTGATGAACA
TGATGACCGCTAACGTTATCGCGATTACTTTAAGCCGTATAGCCAGGTA

Contig 27 (500 bp)

AGCTGGATGCCCCAGCTGTGGTCCCTTCCCTTCCCTCAGGGCAGGTTCT
GTCCCTCTTGACGCCACCGTCACTGCTGTGGACAGGTCTGCACACCCGCC
GTCCACCAAGAGCGTGGCAGGTCCCTGGGCACGGGCCGGCTCCTGACGCA
CCATGTGTTCAAGGCAAGAGCACTGGACAGAGGGTCCAGACGTCCCTTG
TCCTGCTCAGGCTGGGCGGGGGCAGCCCTGGCGGGAGAGGCCCTGGGCA
TCAGAGCCTCTGTGGCTGGAGCTTGGCGCCCTGCCCTCCCACTCCGT
CTGTCTCCTCGCCGCGCTGCACGGACCTCTCCCGGCCCGCCAGGCTCATT
ACTCTTAAGGACCCCTAGCCCCCTATGCTGAAATGCTGTACCTCGTGCTTG
TTTTCATCTGTTTATTACCTTATCTTCATTCTGCTGATGATATCTGGT
TATTCCTTATTGATTATATATCTTGTTCGTGTTTATAGGACACTGT

Contig 28 (450 bp)

AGTGGGTTCGGGCGCTCCTGACGCTCAACACCGTATTTCCAGCGGACCGC
GGATTCAACCTGGTCACACGGACGCCATGTAGACATGTTCCGGGTTACGC
GCAGAGAAGCGACCTGCTCAACCGGCTGGTGAAGTCGGGCGCTCTTCGCCC
AGACCGATGGAGTCGTGGGTGTAAACCATCACCTGACGCTGTTTCATCAG
CGCAGCCATACGTACGGCGTTACGTGCGTATTCACGAAACATCAGGAAGG
TGGAGGTGTACGGCAGGAAGCCACCGTGCAGGGAGATACCGTTAGCAATC
GCGGTATACCGAATCGCGAACACCGTAGTGGATGTAGTTACCCGACG
ATCTTCGTTGATTGCTTTAGAACCAGACCACAGGGTCAGGTTAGACGGCG
CCGGGTACGAGAACCGCCGAGGAATTCGGGCAACAGCCGGACGAACGCT

Contig 29 (450 bp)

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TCAGGCCAATCTGTCTGGTCTCCAATGGGACAATTGGTCTTTAGGCT
TCTGTCCAATGGTCCGAATGGCCCACTCCCGGGCGCCGCAAGGGTCC
TCTGTGCTCGGGTGGGTGGCAGGACCGCCCGAGGGTCTGCCAGCC
CCGTACCCGGGGCCAGAACTTCGGGCTCTAGCTGGCTAGTCCGGCTG
CTGTGCGAGGGGGCTGCGCTGGGGGAGAGGCGGGGTGAGGTAAACCTC
CCAGCCGCCCGGGTCCCTGCCGAGCCCTAGGCGCCGAGACGGTGGCTG
GGTCGGTACCGCCAGACCCGAGGGCTCGGGGCGGGGTGACCCAGCTG
TCGCACACGCTCGAGCTCTTGTCTCATCAGGGCTCATCCCTCTGGACC
TCTCTACTGCCCACTCACCCGCTGGACCCATGAAGCCCGCGGA
Contig 30 (600 bp)
TAAACTAGCTCTAGTAGAAACATTTTATTTAAAAATAAAAAACCTGACT
ACGTGCGGAGTTCCCGTTGTGGCTCAGTGGTTGACGAATCCGATGAGGAA
CCATGAGGTTGCGAGTTTCGATCCCTGGCTCGCTCCGTGGGTGAGGATC
CGGCGTTGCCGTGCGCTGTGGTGTAGGTTGCAGATGAGGCTCGGATCCTG
CGTGGCTGTGGCTCGGGGTAGGGCGGGCTACAGCTCTGATGAGACCC
CTAGCCTGGGAACCTCCACATGCCCTGGGAGTGGCCCTAGAAAAAGGGCA
AAGACAAAAAACAAGAAAAAGAAAAATAAAATAAAAAAGACTATGT
AAATGAAATTAACGACTGCCCTAGGGTGGGATTACAGCATGGGAAGTACA
GCATGGCCGTGACAGTCAAGGCTGAGGCGGGAAAAATGGAATAGGTTAG
GTGAGTTTCTCTGCTATTGTGATGTGGTCTGCTATCGCTGAAGACGG
ACTGCACTGAGATAAATATGTACAGTAAGCATCCGAAAAACGCCAGAAC
GGCAAAACGAATGACTCCAAGTAAGAACCCAAAGAGAAAAAGGAATAAT
Contig 31 (450 bp)
GCGCGGGCGTTCCGGCTGGGTATTTAACGTGGTCACCGSTTCGGCGGGC
GGGTCGGTAACGAACAGCAGTAACCCGCTGGTGGCAAACTGTCTGTT
TACCGGTTCGACCGAAATTTGCCCGCCAGTTAATGGAACAGTGCAGGAAAG
ACATCAAGAAAGTGTCTGCTGGAGCTGGGCGGTAAACGCGCTTTATCTGTC
TTTGACGATGCCGACCTCGACAAGCCGTGGAAGGCGCGCTGGCCCTCGAA
ATTCCGCAACGCCGGCAACCTGCGCTCTCGCCAAACCGCTGTATGTGC
AGGACGGCGTGTATGACCGTTTTCGAAAAAATTCAGCAGGCAATGAGC
AAACTGCACATCGCGCAGGGCTGGTAACGGCGTCAACATCGGCGCGCT
GATCGATGAAAAATCGGTATCAAAAGTGAAGAGCATATTGCCGATGGCG
Contig 32 (450 bp)
GGTGGATGCTGGCGATAGCGTCATCTCTGCTTATGCCGTGCAGCGGGCAA
GGATAAAGCGCGGATAAACATGACCCGCGCATCAGCCCATGCCCGCAGA
GTACGGATTACCTTCCCGGTGAGCGCCAGCGTGTATGCGTGCAGCGCGT
GATACGCGCGCTAAAGCGATGGTGGCGCTACGTTTGGTGGCGCGCGCG
GGGATTTTACCGCTTTTCCACCGCTTCGGAACCGGTGTAACAGCAGAG
CGTTTTCTTGGCGAAATGCCCGCACCTTCTGATTCAATCTCGCACA
GCTCCAGATACGGCTCGTAAGCAGCACCTGGAAGCAGGTGTGCGACAGT
TTTTTCACTGCGCTTCCACCGCGCCACCACTTCGGATGCAAGTGCCG
GGTATTGAGCACCGTAATCCCGCGCGAAATCAAGATACTACGCGCTT
Contig 33 (500 bp)
ACGTGAGGTTTGGGGAGGAAAGCGGGGACGAGCAGCCGAGAGGAGTG
GGGCTGGCTGTGGCTGATGAACTCTGAGAAGGTTAAGAGCCCCATT
TTTGTCTTCTCTTTTATTATGAAAAATTCAAATGGATGCAAAAGTC
CCAAACCTAACTGGACATCTTCTTGGTACCAGGAACGGTCAGGCACTTAT
GATGCACCGAGCCCGAGGGAAAAACCTGCCGTCTGGAGCCACGGTC
CAGCAGGGCACACAGGCCCCAGCCCGCAAGCGCACGGCTGAGTCAGTGA
ATGGCGTGGCTCTGGTCAAGGACGGGCACTCTGGACCCAGGGGAAGCT
CTGAGGAGCCCCCTTCACAGCGTCAAAAACTGTTAAGAGGGCCATGTTGC
CACCCGCCACACACGTGGTTCAAGAGCAGACCCAGGCATCGTAATATG
TCATCCGTGAGTTCCCTGTGTGCCACCAACAGAAAGCCCATCGTCACGTT
Contig 34 (400 bp)
CGGCATCGATGTACATGGTACGCAAGGCACTCGTAAGGCCCGAGCCTCT
AGGCCCTTGTCTATGTACAGTCTGCTCGCGGGGATCAGCAGCCAGGCTTG
TGACCCCGGCCACTTTGACAGATAAGGACACAGAGAGGCCACAGCACTGG
TGTAGGGCCCAAGCAGCAGCCAGGGCAGGGAGGACTGGGTCTACCC
TGCCCTCAGTGGGCCAGCCTCTCTGGGAGTCCCGAGTCTCCCACTT
AGGAGTGTCCCTGGAACCTCTTCTCTCCCTTCCCGCCTCACCCGGAC
CCCCGCTCCCCCACCACCCCTCCCTCTCTTTCACCTTGAG
CTCCCTCTGAGGACCTTACTGTCTCTGCTTATCTCCCTTTGAGCCA
Contig 35 (500 bp)
TGGCGTGAACTATGTCTGCGTGAAGAGCATTTGTGGTGGTAGCGCGT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TATATGCGGGAAGTTTAGCGCAACTGGACAGCCTGGGTTTATCCGGTAGC
GAAATCCGCTTTACCGGTAAAACGCTGCTAGCGCTGGTGGAAAAAGCGCA
GACATTGCCGGAAGATGCCCTACCGCAGCCGATGCTTAACCTGATGGACA
TGCCGGGTTATCGTAAAGCGTTTAAAGCGATTAAAGTCGCTGATTACTGAC
GTGAGCGAAACGCATAAGATCAGCGCCGAATTGCTGGCATCGCGTCGGCA
AATCAACCAACTGCTGAACCTGGCACTGGAACCTGAAACCGCAGAACAATT
TGCCGGAGCTGATTTCCGAGCTGGCGTGGTGAAGCTGATGGCGGAAGCATT
ACACAATTTATTGCAGGAATATCCGCAGTAAATCTTCCGAAGCCGAGCT
GGGCGGCTCAGCGCCACATCCGGCTTCGGCAAACTACAAATCCAACACC
Contig 36 (500 bp)
GATTTACAAGCCTGACCCACGCGAAATGCGCTAACAGCGTAAAGTCGT
GCGGCCAGAATTTTTCGTCTCTCGCTTTGCGTCAATTCAAAAGTCAGC
GCTACGCCATCAGCATCTTCATGATGTGATTTACGCGTCCACGGCAGGTT
GCGGGCAAAACCGTGCGCAGGCAGACCTTGTGTGCGCCGGACCAAAACC
ACGGCCAGCAAAACCGGTACGCCACCGCAATAGCGACGCCATTTTGAAC
GGTGTGTGTGTGCTCAACACAGAATCTTCTTACCCCGCAGGTTTCCA
CGAGAGAAGGTGTGCGCCCTGTAATGCAAAAGAGGCTTTTACCTGGGGAT
GATCGACCAATGAGGTCCAGTTTATCCAGTTTACGACGGGAGGAGACA
GGGAGATTGTGTGATGACCGGAAGGGCAAAATTTTCTTAATCATGAC
GCAGTCTTTAACTTCATTTTATCAGGTAAAAAAGAGCGACCGAAGTC
Contig 37 (300 bp)
ACCTGATCAGGCTCTGCACTGTGTTTCATCAGCGGAGCGGAGATTTTGAC
CGCCCCATGCATAACGGAAGGCGTGGGTAAACCCCGGGCGGCTTCTT
TATCAAGATGACGTTTCAATATTCGGCAGGTGCAAGTTGTTTATCCAG
AAAGCGGTGAGCGCGTATGAATATAATCTGTGGGATTGAAGCATCCT
TTTCCCTCTTTCGGTGAATGCGCTGAAACGGCTTATTCAGCGGTTCA
GGGTACGCTGATAATTTGCAATTTAAATACCATTTATGGGTACTTTT
Contig 38 (450 bp)
ATCCTTTTGGGCTCTGGCAATTACGCAATAAAGAGGCCCCCATGCGATT
AAAGTCACCGGCCACTGTCTCTAATCATGGAGAAATTTCCATCAGTG
CGGTCTCGATGCGCAGGGATTGCTCTCGGTTCTGCTGGGATGTTAGCG
AAAACATTGCCAGTGGTCAATTTAGTGAAGTGTACCGGAATATTACCAG
CCAGCGAAGCTGTGCTCCGTTTATGTTTCAAGGCTGGCGACGTCAGCGAA
AGTGGGATAACGGTAGAGTTTACGCCAGTATTTGCGGAGCACTACCC
GGAATGTTTCACTGTGATGCGCTGATTTATGATTCAATTATCGGGTTGA
TATCAGTTTAAACCTGATTTTCTCTTTCTAAGCCGCTACAGATTTGGT
AGCATATTACCTTTAATCGCGCATGATCTAAAGATAATTGAAGAGGTTA
Contig 39 (450 bp)
AATGTACTGGCAAAAGCCAAATGGCGAAGCGTGGGGAACGTTACATGCTC
TGCTGGCGGATATTAATAGTCAGGGTCAGGTGCAGATGGCGATGAACGGC
GGCATCTATGATGAAAGCTATGCGCGCTCGGTTGTACATCGAAAACGG
TCAGCAGAAGGTGGCGTTAAATCTCGCTTCAGGTGAAGGGAATTTCTTTA
TCCGTCCTGGCGCGGTGTTTATGTGCGGGAGATAAAGTCGGCATCGTT
CGTCTGGATGCTTCAAAACCAAGTAAAGAGATTCAAGTTGCGGTGCAATC
AGGGCCAATGTTGATGGAACCGGTGTAATTAATCCGCGTATTCATCCCA
ACGTGCGCTCAAGCAAAATTCGTAACGCTGTTGGGATTAATAACATGG
GAACGCGGTGTTTTGTTGAGCCAGCAGGCAACAAATTTTATGATTTG
Contig 40 (400 bp)
GACATTAATCATTTCAAAATCAAAGCCCGGTTTCCATCGCCCGTTTGG
TGGCGTGGCACTGAACGCAATCGTTACGAGTGTAATAGTAATGCGCATG
ATTCTGATTTCCGTTTAAATGAAGATACGGCGCATGATACCGCTCGGG
TTGTCTCTCTGTGATACAGAGATACTAGATGTAGTTGAAAAAGATTCA
ACCACACAATATATAGCCAGTAGGGGTGAAATTAACCTGGATATGAGC
GTGACGGGTAGGGGATTTTGTGATTACCGGCAAAAGAAACCCCG
AAGACAGGCTTCGGGGTCAAAGACGCGTATTTATATCATTTTGCATA
CGATTTGCGCATGCTTAACAGTGGCGGATTAATATCTACCGCAGCTG
Contig 41 (500 bp)
GCAAAATCACGTCCGCGACCTGGCGTTGTGCTGGGCCATATTGGCAAAG
GAGCTGGATTGCGGTGCTGCAAGTGCCCTGAATAATGCCATTGTCTTG
TACCGGAAGAAACCTTTGGAATGAACCCACAGCAGCAGCTAAGCA
GCAGCGTGCTGAGTGCCACGCTTAAGGTACGCCACGGATGATTCAGCACT
TTCCCGAGTCCACGACCATAGCGGGGATTATCTGTGCAACATTTTTC
CGAGGCAGGGAGAGCGGTTCTGTTTACGCAACGACTCTTGCTGAGCA
TCCGCGCGCATCATCGGTGTGAGGTGACGACACACCGCTGAGATC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

AAAATCGCTACCGCCAGGGTAATAGCAAATTCGCGGAACAGTCGCCCCGAC
GATATCGCCCATAAACAGCAGTGGGATCAACACCGCAATCAGTGAGAAGG
TCAGCGAGATAATGGTAAAGCCGATTTACCTGCGCCCTTGAGCGCCGCC
Contig 42 (400 bp)
AGCTATCTACGGCAAAAGGCACGGTAGTCAATTCGTTGTTAAATACATC
AAGCGTTTGGCGCCGAAATACCATCTGCCAGATGCCATTTCAATTCGTAG
CGCACTGCATAACGGCTACCGGATGCAGTACGTAAACCCGAACCTGGGGC
CGGAAGGATTTAGCTTTCTGCAATACACCGCGCGCACCACTGGTGTGGC
GAAAGGCGCGATGCTGACTCACCGCAATATGCTGGCGAACTTGAACAGG
TTAACGCGACCTATGGTCCGCTGTTGCATCCGGGCAAAGAGCTGGTGGTG
ACGGCGCTGCCGCTGTATCAGATTTTGGCCCTGACCATTAACTGCCTGCT
GTTTATCGAACTGGGTGGGCAAGCTGCTTATCACTAACCGCGCGATA
Contig 43 (450 bp)
GATTAGCGCCAGATGCTCGCCATCGAAAAGTTGAATCAACCCAGCTGCC
GGTAATAAGTGCGCGTACGAACAAATTCAGTATCCAGGGCTATCGCCGGA
AAGGCACGGACGGCTTCACACAAGAGCCAGCGCATCGTCCGTGGTAAT
CATTGGTAATTCAAATTGTTTCTCTTAGTGGGCGTCAAAAAAAGCGC
CGGATTAACCGCGCTTCGACGACTGACTTAACGCTCAGGCTTTATTGTCC
ACTTTGCCGCGCGCTTCGTACGTAATTCGTGCGAAAATTTTCCGAC
GTTAGATTTCCGTAACCTCATCAGAACTCCACAGCTTCGGTACTTTGT
ATCCCGTGAGCTGACGGCGGCAAAAGTCACCACTGACTCTTCGGTAAGC
GATGGATCTTTTCACTACGAAGATTTTACCGCTTCACTAGGAGCC
Contig 44 (750 bp)
GAGCAGCCCCGCTGATGACAGGCATGCGCCCGCTGGGCTCTCTCTCT
GGTGCACTGAGTCACAGGATGGCGCGGTGGGCGCGGTGGTGAAGCGGT
CCTGGAGGGCTCGGGAGGGAGGATGCGCTCAAGCTGGCTCCCGTGGGGC
TGGCCCGAGTAGCCTCCGTGAGGGCACCGTGTCTGCTCCAGAGCCGCG
TCCCGCGCTGCCCTGCCCTCCCTTCCCTGCCCGAGTTCCCGGAGCCCC
TGGATCCCGATGGGAGGCGCCCCGAGGAGAGGGGACAGGGAGGGGGCCC
AGAGCTCTGAGGCCACAGACCTGGCCAGGACCTTCGTGGGAAGAAGAG
GTGGGCCCCAAAGGCACCTACAGAGAGGGAGGCTCTGCTGGCTGGGGGGC
CTTCCAGCGCGGGCTTCCAGCAGGGCCAGTGTCTGGGGGTGGAGGGA
GTCCCTGGCTGCTGGGGGGCGCAGGAGCACCTGGGCGCTCTGGAAGAG
AGCGGCAGGAGACTGGAGCCAACTGGGGGGCAGAGGAGGGGTCCAACCC
CAGCGGTGGTGTGGGGGTGCTGGTGGTGGAGGCCCTGAGAGGCTGTGCT
GGGGGGCAGAGCGGGTGTGGGAGGGGAGAAGGGTCCCGAGGGCTCATG
GGCCCTTCGAGCAGTGGCAGTTGGGTGGGTGGCTGTCTTAGGGCTGT
ACCACGGTGGGTGCCCTGGAGAAAGAGTCTACCCCTAGTCTTTGCTGCA
Contig 45 (300 bp)
TGGGACCCCACTCCAGCCCCACTGAGTGACGCGCCCCCTGTGGTCCCA
CCGCCAACCCCTGCCTCACACCAGAGGGGTGTGGCCACACCTTGTCACA
GCCTGTCCCTGAGACCACGAGCCCCGGGCTCAGCCCCCTCCTCACCCCT
GGACCGAGGAGAAGCCCCACCTGGGCTCAGCTCTTGAGCTAAACTTCC
AGGAAGGTCTGTGTCCTCGGGTCTTAGAGCATGGTGGGAGGGGGATG
CTGTGGGGGCGCAAGCCCTCCCCACATTTGCACTCGACCCGGTGGNG
Contig 46 (300 bp)
CCGGCTAGAAGCCACGAGAGCCCCAGGCCCGCCGACGTCTCTCCTGC
AGGGATTCCGCAGCCCTGGGGCCACAGGGCCTGAGCAGACCTTGGGGTTC
CGGTGTGACTCCAGCCAGGGTCCCTACTGTGTAGGCACAGGGCAGAGTC
AGCCCTGGGACCATGGCCACAGCTGCTCCCGCTGAGCCGGGCCCCCGC
CCAGGCTGGGCCCCCTCAGTGCACTGTCCCAAGCCAGCTGCTCTCCCCAC
CTCCACCTTCTCCATCCAGTCTGCCCCACGGCTTTGCTCAGGCCAG
Contig 47 (500 bp)
TTGACTGGCACTAGCACGAGCTCTGTACCCGGGATCTGGGCTCGGGAGA
AGGGAGACCCCCACCCGGCAGGCCGAGGGCGCTGTACACCATGACTCT
CAGCCTTCCCCACCCGACGGAAGAGTGACCTCTCCCAAGCCCCCACT
CAGCCAGGACCGCACACCCGCTGAGTCTGCGAGTGGGGGCGGCTCAGGG
GCCCGAGTCCCAAAGGAGTCTGCTGGCCCTGGGGGGAGGGGAAGCAGC
AGGGTGGTACGGGTCTCCCTGGTTGGCAGGACCAAGCTCAGCCCGCT
GCCTCCAGAGGGCAGCCGGACACCAACAGTCCGGGACCCACGTACC
TCAGCTGCTGCAAGTGCCTGTGCTGACTGTTGCAATGGGGCGCTGG
GTGCTCCCATGGACAGCTCGCCACTCATCCAGCCGCTACCCCTTCC
GGGTCCAGTGTCCGGCCGCCACCCGCTGCCAGCCCTGGCCTCCTTC
Contig 48 (500 bp)

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GGGGTTGCCGAGGCTGCTGTGTAGGTGCGAGACGAGCTTGGATCTGGC
GTGGCTGTGGCTGTGGCTGTGGCTGTGGCATAGGTCAGCCACTGCGACTC
CGATTGACCCCGACCCGCGCACTCCACATGGCACAGGTGCAGCAGGG
AAAATAAATAAATAAATAAATAAAGGTGAAGACAGTGGATTTCATCTCT
TGGGGTTGCGGTAAGCTCTACACAATAGGGAGTTTACCATTTCCTGT
TCAAGTGGCACTGAGTCAGCTCAGTCCTGAGGGCCACAGATGCCGTC
TGCCTGGGAGATTGTTCTCTCACCACACTGCCCTCTGTCCCCACTAAA
TACTCACTGCCCTCCCGTCCCAAGGGCCCTGCCACCCCTCTGCTTCC
TGTCTCTGAACCTGCTGGCCACGAGGACCGTCTGGTGACCTCACTCTTC
GGCCCCATTGTGCGCACACCCACTGGCTCTCCCCGGCATGGGCAGAN
Contig 49 (600 bp)
GGGATATTGGGGGCATATTGGGGGGAGATCCCCACAAGGCATTGGG
GTTTGTGGTTTGAATGCCCGGGCCGATGGAGGGGGCCGGGAAGAA
TCTAAGCCTTACTTGGGGAGGGTTGGGCCCGGGGCCCGGGCCGAAAT
GCCCCAAAGACAGAAGGTGTACAAAATTCTCAAAGGGTGACCTTAAT
GAAACGGGTCCCGTTGGAAAGAGGTCAACAGGGTGGATTGGTGGCACCG
CAGAATTACGACATTGGCTCTCTTCAATGGCCGACGCTGGGGAT
AGGGCCCCCGTGAGCGCGGGGTCTCGGTGGGACGGCGGTCAAGGGT
CGGTGACGCTTGGCTCTCTGACCGCTCCAGCTCCTTGGCGAGCGTGGC
AGCGCGCGGGCGCGCAGGAGGGCGCGCAGCGCCCTGCGCAGGCGTTGG
GCGGACTGCTTCCAGGTGTCTATAGCGGAAGAACTTGGCCACGGGGTATCT
GGGGAAGTTGTCTGAGAGGGGAAGGGCCCTCAGGGGGGGCTTGGCCC
CCAGCCCCGTCCAGAACAAACCTTTCGGGGTCTCTGCTGCTGCC
Contig 50 (179 bp)
ATCTTCATATTATGACAGACACTCTCTGCTTTCTATCTTGGGGAA
AAGGACGATGTCACTTATGCAATAAGCCCACTTGTGGCCGGGGCTTGA
CATTATCTCTCTGCTGCTGCTGCTGACCGTATTGAACTGAGTTAATGG
GCAATTTGATGAAGTAACTGCCACC
Contig 51 (500 bp)
CTCGGGCTGCTTCCAGGGGCTTGGGAGCCATAGAATGCTATGGAGCA
AGAGAGTGCTATGGTCAGACGACTTGGGGGAAGGTCTGGGAGAAGAGGG
GTGACTGGCCACTGTGATAAAGAGTGGGCGCTTCTTGAGATAACACGGT
GGGCGCCGAGGTGGACCTGTGACAGTGGAGAAGGGCTCTGCGCGGGCC
ACTACGTGGCTTGGGCTGCCGGACAGAGAAAGCCCACTTCCACGGCTG
CCTCCAGGGCGGCTTCTCTCTTCAACCGCGGGCCATGCCAGGTGC
AGGTGCCATCAGAGGGTGTCAAGAGAAGCTTGGGCTGGGGTGTCCCA
GGTCCCGGAAGCCCGTGTCCAGGGGCCACTGAGGAAGCGTGGGCGCA
CAGAGACTGTCCCTCGGTGCTCAGAGAGGGTCCCGTCCCCACGGCAACGA
CGCCCAAGCGGAGGTGGTCAGAGGTCTGGGAGGGAGGATGGCCCGCA
Contig 52 (900 bp)
TGTGTTGCACCTGTTGCTGCTGCTGACTCTAGAGGATCAATACTCCTTA
CATAATTAAAGGAGAACAAATGGAACCTTAAAAAATTGATGGGACATATT
CTATTATCCCGATTACAGACAAGCCTGAAAAATGGAACATAAGTTATCG
GATATTCTACTGTTGACTATTGTGCCGTTATTCTGGTGCAGAAAGGCTG
GGAAGATATAGAGGATTTGGGGAACACATCCCGATTTTGAAGCAAT
ATGGTGATTTGAAATGGTATTCTGTTACGACACCATTTGCCAGAGTT
GTATCTGTATCAGTCTTGCAAAATTTACGAGTGCTTTATTAACCTGGAT
GCGTGAATGCCATTCTCAGATGATAAAGACGTCATTGCAATTGATGGAA
AAACGCTCCGGCATTCTTATGATAAGAGTCGCCGAGGGGAGCGATTCTAT
GTCTAGTGGCTTCTAACAATGCACAGTCTGCTCATCGGACAGATCAA
GACGGATGAGAAATCTAATGAGATTACAGCTATCCAGAACTTCTTAACA
TGCTGGATATTAAGGAAAAATCATCAACTGATGCGATGGGTGGCCAG
AAAGATATTGCAGAGAAGATACAAAAACAGGAGGTGATTATTTATTCGC
TGTAAAGGAAACAGGGGCGGCTAAATAAAGCCTTTGAGGAAAAATTC
CGCTGAAAGAATTAAATAATCCAGCGCATGACAGTTACGCAATGAGTGAA
AAGAGTCACGGCAGAGAAGAAATCCGTCTTCATATTGTTTGGCATGTCCC
TGATGAACTTATTGATTTCAGTTTGAATAGAAAGGGCTGAAGAAATTAT
GCGTGGCAGTCTCCTTCCGTCCATAATAGCAGAACAAAAGAGAGCTC
Contig 53 (450 bp)
CCAGCCACGAGCTGGACCTCCCGAGAGGGGCTGCTCTCTTCCCGC
CCAGACGCCCCCAGCAATCTGTGGCCAGAGGGAGTGATACCGAAGATG
GCCACATGGGGCGCCAGCCACAGGGAACCCAGGAAGGCGTGGACCG
TCAGGAGTCAGGGCTGCTGTGACCCATGTGGCTGGGGACTTCCACAG
CCTGGTGGAGATGCGCGGCACACCGTGCCTCGGGGAACGTGCACACG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GGTGGTACATGTGGCCGGAGCCAGGGCACAGGGTGAGGGGAGAAGGGAG
CATGCGGGTGCAGACTCGGAGCCCGCGCTGAGGTGCTGGGTCTCTCAGGA
CACGCTCTGGGAGTGGAGGACCCCATCCACGCCCTCACCCAGTGTGTGC
CCGCTGCTCCCCGGAAACCTCAGACACAGAGGGGCACCCAGCCCC

Contig 54 (1133 bp)

ATGGCGCTCATTAGAATTGACCTCGGTACCTTGGGATCTTTTGACCCCT
ACCTCAGCCATCTACAACATTTACCTCCGAATGAATGAGAGACACCAAA
AGCAAAATTCATAGAAGAGAAAAAAGTAACCTGGACTTTAAAAATGTAA
ACTTCTGCTCTTTAAAGGCAGTGCTAATGAAGTTCAAAACAAACCACA
GACCATAAGAAAAATACTTGCAAACTTGTCTGACAAAGACTAGTGTTC
GAACATACGACGATCAGGGAGAGGAAAACAGCAATCCTATAAACTGGA
CAAGAAATTTGGGGGAAAAAAACCCACTTGGCCAAGAGTGGTAAATA
AGGCCATGAAAAACATGCTCAACATCATGAGTCATTAGAAAAATCAAATT
AAAAATTATAATGAGATACTACTACACAGCTATTGAATGGATAAAAAATG
TTTTAAAACTGATTATACCCAGGTTTGGCAAGAACATGAGAAACGAGAT
TTTCACACAGGATTTGGTGGAAAACAGAAAATGGTCCACCCACTTTGAAA
AGAGCTGGGCACTTCCCTCAAAAGTTAAACATACATCCAGGACCTCACAC
AGGCTTTCCACCACAGGTGTTTATTCAGAGACATGAAAGCGCTCATCCA
ACAAAGACTCGTAAATGAAGGTTTATAGCACCGTTTGTGGCCCGAACTG
AGAAAACCCAAATGACCTTTAACCAGAGAAATATCTAAACAAATATCCAT
TCACATTAAATCAACCCATAAGAAGGAACGGCTATGGGACGGGAACCGTA
TTGAAGAGGGTCAAAATACATACGACGATCAAGAAAGCTGCCCAAGG
ACACCACTGCAGGGTCCATGGACTGAAACTCGAGAGGTGAAAACTCG
CCAGCAGTGACAGAGAGCAGGTCCGAGATCAACCTGATGTGGAGGAAATG
GAACCTCGTGGCTTGTGGCAGGACTATAAACTGGAGCAGCCCTACGG
ACAACAGTAGCCCGGGCTCTCTCTCTCCATCTCCCTGGGAGCCTGAGCC
TTGAGACGCTGGGGCAAGTGACCGGATGCTGCTCAGCTGGGGCCCCGG
TGAAAACACGTGGCAGCTGGGGAAGAATCGTA

Contig 55 (735 bp)

TACTGCCTGCTCTATGGACTTGACTCCTCTCGGGACTTCATGCGAGGGA
TCTTACAGAAATTTGTCTTTTGCACTGCGCTTGTTCCTGAGCATCGTG
TCCCCAGGTCCATCCATGTTGACGCTGTGTGAGGATTTCTTCTCTTT?
CAAGGCTGAATAGTACTCCACTCTGCGGATGGACCAGTTTTGATTATCC
ATACTAGTAAATCCATACTAATACTTGTTCCTGAGGCCACAGCTTAT
GCTACCTTCCGTGGGCTCCTCCCTGCGCTGTCTACGCTTCTGTCTATA
CCCCCATCCCTCTCATCCAGGCCACGCTCTCTGCTCCCTGGACACTGTG
CCAGAGGCCAACTGCCCTCTGACTGTGTCTCTCGGCTGACGGAGGACAAG
CCAGGCTCAGGGGTCCACGGGCTGGGGCCCCAGGGCTCCCATGGCTGGT
GCCCTTCTCTGATCCAGAAAGTACAGTGGCAGCAGCTTTCAGCTGC
CCACCTTCTGTCCGAGGCTGCTCGGGTGGGGCAGGTGGGCAGTGATG
TCACCTGCTGTAAACCCCTACCTCGGCTCATCCCTGTCCAGGAGGTAC
GGTGACCTTGGCAAACTTCTGAACAACACACACCTCCCTGCTTAGAG
GCCGGGGGCTCCCGGGTGAAGTGGGGCACAGGCTGACCCAGCCTGTCT
TCTGTTCTCTGAAGGACATGATAAGTACTGCAACA

Contig 56 (500 bp)

AGGAAGAACAGGAAACAACGGGTTGAGGAGAAGAAACGGGTGTCTGGCA
GGGGCACGTGCCAACGGTCCACGGGTGCTGCCGCGCTGCGGCTGGCGC
CAGAGGGGGCAGCTCCGCCCTCGGGCCCGGCTGCCGCTTGTGTGGC
TCGCGGCTGGGCTCTGCTTGGCTGGGTACAGCTGGGTGCAGCCGAGGC
TGTGGTGGGTGCCCGGGTCCAGCCAGCCCGGCCACCCGGCCGCTCTC
GCCGGCTGGCCGGGCGAGCCCTCCTGAGTCCGAGGAGTCCGCTGACGG
GCTGATTGGTCCACAGCTCAGATGCAAAACAGCCCACTGCTGCTGGAGC
CAGCCAGCCCGGACACCTTGGTGGAGGAGGAAGGAGCAGCCTGGAGA
GCCGCGCCGATGATGCTGCGGGGAACCGGCTCCCGCGGGGGCGGCC
TGCTCTGGCCAGGCTTGGCTTGAATGCTGAGTGGAGGTTGGCCCTATA

Contig 57 (500 bp)

TGGCGTTGCAGTGGCTCTGGCGGAGGCCGGGCTACAGCTCCGATTGGA
CCCTAGGCTGGGAACCTCCATAAGCTGTGGGTGACGCCCTAAAAAGCAA
AAACCCCAACATATATATATATATATATATATATATATATATATATAT
CATAAAATAGAATTTACCTTCTTAATAATTTTCAGTGACAAATTCAGTGG
CACTAAGCACATTCATGCGGCCGTGTCACCTGCTCCAGAACTTTCCATCT
ACCCAAACGGACTCTCGGCCCATGGAACACGCCCTGCCCCCTCCCCG
GCCCTGCCCGGCCAGCTCTCCCTGTGTGTGGATCCGGCTCTCCAGG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GACCCCGTGGCTGGGCTCACAGAGTGTGTGTCCTCTGTGACCGATCGTC
GTGTCCCGAGGGCCGTTCTGTGGCAGCTGCGTTATGACCGACTACCTTC
GAATGCTCAGTGACTGCGGTGCATTGGACACGCAGTCCGCTACCCCTTTTC
Contig 58 (550 bp)
TGCTTTCTGTGCCCCCTCCAGCTTGGGACCCAGCAGGGCAAGGGGTGT
ATAGGGCTTAAGGAGGCAGGGGGCGTCTCCTCCCGTGGCTGCCAGAGC
ACCCCGAGCCCGCTGCCCTCGTCCATCTCCAGCTGTCTTTCTGT
GCCCTCCCTGTCCCGGGCGGGCCGACACTGGCTTCCACCTCCCCACCCA
ACTGGCGGCCGCTCTCTGCTGAGGCACCCGAGGTCCCGCTGCTG
GGGACCACTGGCAGTGGGTCCACTGCTTTCTCAGCGTGGGCTTTGGA
GGGGGGAATCTGCACATACCATCCCTTCAGGCCCGTGGGAGCCTGGGA
CCATCCGGGACCCCTGTGGGCAGGCCAGAGACTGCCAGGAAGAGACCC
AGGGGACCAAGGCAGTCCAGGCCCTCTCAGCTTCAGGCCAGGGGAGCCCA
CCCCAGGTGGCAGGTGAAGCCAGGCCCAACCCACAAAATGCCCGCA
GGGAAGTAGGAGGGACAGGAGGAGGGGAGGCCAGGCCGGGGCGCCCTTG
Contig 59 (800 bp)
TGAGGAGCGCAGGCCAGGCCCTGAGTGTGCCAGCTTACACCCCTGGCAG
CTTCGTCCCTCTTGGCCCTAACCCCATCTACCCAGCAGCAGGGGCTC
CCCGGTGGGGCTGTGTGAGCGTCTGACTGGGGTTTGGAGTCAGGTCTGC
TCCAGGCTCAGCCCCCATCCCAAGGGTGCCCTGCAGCACTGCTGCCAC
CCCTAGCGCCCCCAGACCTTCGCCCTCCAGCTGGATGTACCCACGGA
CCCTGAAAAGTGGGGCTGAGCAGGTGCCCTGGCTGGAGTCCCCTGACT
GGGGCTGGCCAGGCTGCCCTGGAGGGCTGTGGGGCACAGCTGCCCA
GGGGCCCGTGGGCACTGGCTCTGGAGCTGACGACAGGCAGGCCCTCTCT
TCTGGCGGGGCCACACCTGCCCTGGGGTTTGGGGCAAGGCGGGCAGC
CCCATGTACGGCGGGGGCGAACCAGGTAATTACAGCCTGGCAGGCCGCT
CCCGAGACCCCGAGCCCCGAGGGGCCCAACCCAGGCTGTGCCACCAAGA
CCTGGCATCCAGGGCCCAAGCAGCTCAAGGGCAGTGTACAGATCTTT
TTAAGTTGAGACAGAATCGACACATGACAAGTTCCTGGTTTATGGTACTT
CGCTGCCGGGGCCGCGCAGTCAGTTAGTGACCCAGCACACCCACACAGG
TACAAATGCTCTTCAAAGAGGCCCTGAGAGAGCGCTGTCTTGGCT
CAGGGGTAATGAGCCCAATGGGTATCCATGAGGTTGCGGGTTCCATCCCC
GGCTCGCCGCTTGGTTA
Contig 60 (500 bp)
GGCTCAGGAAGCGCAGGGGCGAGCTGTGGGGCGACGGGAACCATGGGGT
CTGTCTTCCCGCTCTCCTCAAGCCCAACCGCTGTGCCCACTCCGAC
TCTCAGCCAGCATGCCGGCTAGAGCCCTGTGCACCCAGCTGGTGGCT
CTGGCTAAGGGCAGTCTGGCTGTGGACGCGTGTCCCTCCCGAGCAGCC
CAAGGGTCCCATCTGCCAGGCTGGTGGCTGAGGTCTGCCCTGTGTGGTCC
TTGCAAAAACCCGCCCTCTCTGCCCTTGAGGCGTGAGGGAGACGCGG
GCTGGGCGGATGCCCTCGGGCACAGCCGCCCGGGTGGCGCCCTGTCCAG
GAGGGGGCTCCGACGTGCCCTGACGGCCCTGGCCGGGCGGAGAGGGTGAG
GCCACCTCCTGGCCAGCTCCACCCAGCTGCCACGCCCTAGCCAGTGGC
CCGGGGCAAGTCAGCAGAGCCAGGCTTCCGACAGCAGAGGCTGTAGGC
Contig 61 (700 bp)
GATGAGGAAGCCGCTGCTCGTGTCTCGTCTTCTTGGCCTTGGCCTCGT
GCTGCTATGCTGCTTACCGCCCACTGAGACTCTGTGCGGCGGGAGCTG
GTGGACACCTCCAGTTTGTCTGCGGGGACCGCGCTTCTACTTCAGTAA
GTAGCTCAGCGGGGACCGGGGGGGGGGACACAGCAGGTGCTCCATCG
GTGCTGCCCGGTACCTGTGCGGTCTTGGGATGGATGGTGTGGGGGA
CGGGGGGGGGGGGGGGCAAGGAGGACCTCTCCTCCGAGGGTCTGAGA
CTTCAGACCGGGGGCGCCCTGGCCGTGCGCATTTGATTGGCACCTGCCATG
TGCCTGCTGGGGCTCACACCCCTGACGTTCTTGCAGCGTGACTCGAAA
CGGGAAACCGAAGGACGGGTGGCACGGGTGGGAGGCAGACCGTGAGT
GGCAGGCGTGCAGGGGTTCTTTCGGGCGGGGTGGCCAGGCAGGCCCA
CAGGATGACAGCCTGTCCCTCTCTCTCTTGAACCTGCCACAGCCA
GGGCTGCAGGCACTGACATTACCCATGGTATTGTGGTGCCTTGACGTCT
TGGCAGTGGGCTTGGGTTATGGAAGTGGGAAATGAAAGTGGGAATA
AGATGGGGTTTAAAAACCAATTAAAGAAATAAAGGGCGCCCTGTGGGC
Contig 62 (300 bp)
TTTAAAAATTTGAGTCAGTGCAGATTTCGATCTATTCCGCATTACAG
CTCTCTGTTCTCACCTTGCTTGTGCGGATCTTCTATAACCAACACAG
TGACGTTTCAAGGTACTTTATTGAATAATAAGAAAAAGTGACACAAT
CATGTAGTTAACTTTCTGTGCTTTGCCAGTTTGAAGGACCCCTTTT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TTTCTTTTATAGGGCTTCGCCGACGGAAGTTCCCGGGCTAGGGGTTGAGT
CAGAGCTGCAGCTGCTGGCCTACAGCACAGCTCTGGCGGCGATGGATCC
Contig 63 (450 bp)
TCCTGGGCCACAGGCTGCAGCAGCTCACCTGGGGGCTGGGGTCTCGCTCT
GCCGATGGACCCATGAAGGCCGAGCCAGGTGGGGGCCGAGACGGCAGGG
CAAAGGGTCTGCACACACAGCGTCCCCCGACCCGGCTTCTCTGGGTCT
TGGGGGTTGGCGAGGCTTCTCTAGTCTGGGTTCCTGGGAACTTCA
AGAACTGGGAAGTCTTCCAGAAAGTTGGGGTGAGGGGAGGTACCCCCAA
GTGCTGCTCTTCTCCCATCCCCACCCCTGTGTCATCGGCGAGACCCC
GGACCGCCCTCTCCCTGCCGAGGTGTGGGGTCCCCCCTCTGCCGGCCAG
GCTGGGCAGGGGTGAGCGCCCCCTGCTCTGCACTCGGGACTCAGCCTGGG
GAAGCGGGGCCAGGAGGTCTGGCTGGACGGCAGTGACCTTCCACCG
Contig 64 (500 bp)
TGTGCATCCAAACCCAGTGGCCACGGGGGTGACCTCGGCCGGTCAGCC
GCCGCGCTCTCCACGGAACCGGGCTTGGCCTGAGGCAGAAGGACCCAG
GACTCCATCCCTGCCCGGACTCTGCCGAGGGTGCGGTCTGCACAGAGA
CCCTGTGGGGTCAAGCGGCTCGGGCTGGGGTTGAGATGGGATGGTCAG
GGCGGGCCCCGGGGCTGCAGGAGGCTGGGTGAAGGAGGGGGCCAGCT
CAGACGCCCAAACTAGCTTGGGAGAGCTGCAGCCCCGGCCGCTCAAT
GGCGACAGCTTCCACAGAAAGGCAATCAAAATGAGAGACAAATTTGGG
CTTGAAGACTATACCCAGCCAGCTCTTCTTGGGAGCCCAAGCTGCTCCA
GGCCCTCATTGGGTATTAATTGGTTTCGTTTATAGATTTCCATGCTTA
TCAATGGCCACTGGGCGGCTGGGCTGGATGCGGTCCAGGCTTTGTATG
Contig 65 (661 bp)
TCCACGACCTGCCCTCCAGGGCCACATCTGGCGACACCGTCGCAAGAG
TTGGACCGGCTGGTGTGGCCACAGCTCAGGCTTGTCTGGCGGCCAG
GCCGCTCCAGGCTCCAAGGAGCTCTGCTGCCCTCCGGAACCCAGCA
CCCCGGGGCCGCTTCCACCAGACCTGTTTTTCCAGGTCAAGGTACAG
CTAATTTGGGCTTAACTGGACAAGGAGCCCTATCTGGAGCAGGCTCCC
GGCCCTTGGGCTCTGCCCTGGTGGGAGGGCTTCCAGAGGCTGTGTGT
TGGCGCTGACCTGCAGCCCTGAGCTTGAACCCGATAGGAGGGAGCCCC
ACCTGGGCTGGAGCCAGAGAGCCCTCGTTCCCACTCCGAGGGTTCTC
ACAGTCCCCGCCCTGCCCTGGGGACCTGGAGCTCCCGAGCAGGTGAAAG
GTCCAGATGCCCTCTGACTAGAGGCTCTCCGCTGTACAGCATGCTCCCT
TCCCGCACCGAGGACGAGACCTCAGCAGCCCTGCGTGGCTGGGGTGGG
ACCCCAAGGCTCTCTGAGTGTGTTCTAATGGGAGCCGTGGGGCTCAA
CAGTGGGGTGGCACTTGGAGGGAGCCCTCCCAAGCTGCCCAAGATG
GGCCCTGGACT

Contig 66 (500 bp)
TTTGTGGATGAATGAAATCATGAGAAAGTATTGGACCGCCCGTTTCGT
CCAGCTGCTTGCCAGCTGCTTTGTAAGATGACCTCTCACCTTCTCAGAG
GCCTGGCCGGCCGAGGTGGCAGTCACTGAGATGCCATGCTTCTTTGGC
ACGTGGGAGGCCCTGTCCACGGCGTGGGTGCCTCTTGTCTTAATCAGG
GTCAGGGGGAGCAGCAGGTGCAGGGCACATGTGGGGCCGGGGCCGATGTC
TGGGAGGGGGGAGGAGGGGGTGTGCGGAGGCGCTTGTGGGGTGCAGG
GGACAGACCCAGCGAGACCTCCCTGGCCAGGCACAGGACAGGTGATG
GGGGGGCCGCTCCGGGGCTGTACAGAAAGCTCTCAGAGGAGGCCCTCC
CACGGTCTCTGGACCATCAAGGGACCGGGGGCGTGGGCTGGGGGTAC
ACCCAGCTGGCCGGCCAGCCGGGTGGGTGCGAGGCCCGGCAGTTAC
Contig 67 (550 bp)
GGGCAGGAGGGGCCCGGGCTGTTGCGGAGGGTGAGGTGTTGCAAGAGG
GTGTGAGGCAGGGCTCACTGAGCGTGGCGGCTGGCTGTGCCCTAGAGTG
GTTAGCACGTGCCCCACCCCTCAGTGTGCTGTGTTCACTGTGCTG
CTCACAGGTGTGAAACTGAGACTCGGGTGTGTCATGAGCTTCCAGGATG
AGAATCAGCAGGCTTCCAGGCAGGGCTGTCTCCGGGGCTCTGGGCTCTT
ACCAAGGAGGGGACACCAGGGACAGCCCTGCTTGGGGTGTGCGGCTGG
CCAGGCTGGGTGCTCTCTGTGGCTGGCAGCCCTTGGCAGTCAACCCC
TTACCTCAACTGCCCTCAGCTGAGACACGACCTCCCTGCAGAGCCCTG
TCCACCCAGACACTCACTCGCTCTCCAGGAAGCTTCCAGGGCTGCT
CGCCCTGGTCTCAGCAGGAGACAGAGAGAGGGTGGGCCAGGAGCAGA
GGCAGGCAGCCAGAGGGGAAGCCAGGGGCCCTCACTACCCCTGGGGCC
Contig 68 (500 bp)
TTTGCAATCAGCTCGTACCCGGGATCCTTCCCGGGGCTCTGGGGTGGG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GGAAATGGGGGTGAGAGGAGCTGTATCTGCCTGTCTACCTGCTCTCAC
AGGCTGGCCCTGGAGCCCTGGCCTCCTCTAGGGGCACATCAGGTTTGG
GGGAGGCCAGCCACCGTCCACCTCCAAGACCACAGCTGGGAGCCTGC
CCCCAAGCCTAGACCTAGTGGGGCTCTGCCAGCCAGGCCCCACCTTC
ATGCTGCCACCCACCAAGGTGGGACAGTGCAGCCAGGACATCCAGCTTCT
GGAGCTGCCCGAGGCTCAGCACAGGCTGGTACCTAGGGAGCAGGTCAAC
CAGGGCCGCTGGCGAGGCTGCGGGGACGGGGGTAGGGTGGGCAGCAA
AAGAACCTCTGAGCTGGGCCGGGGGGTGGTGGAGGCCGGGGCCGG
GGCTGTGTGCTGGCCCTGAGCCCGTGCAGACGCAGACCTGGGTGGGT
Contig 69 (550 bp)
TGTGCTGCTGTGGCTGTGGTGTAGGCGCCAGCTGCAGCTCTGATTCCGA
TCTCTAGCCTGCGAACCTCCATATGCTGCTCTAAAAAGACAAACATAAAA
TAAATGGGTGCGCTGTTAATTTGAACACTCTGCCTCCTCCAGAGACGAG
GCCGAAACAGGCCTCTCTGAAGGTCCACCTGGCAGGGAGGAGGAGGCCA
GCCCGTGGGGGGCAGAGAGAAGCCGATGTCCCAGACACACACGCACA
GGGACCGTGGCCCCGCTGCCAGCCCGCGGGGGAGGGCAAGGCCAGAG
ACTCCAGCAGCCACAGGACCTTGGTGGCCACAGGACACAAACACAGGT
GACGTTGGGTGAGGCTGGCCTTCCCCCCTGGGCACGAGCAGCAGACA
CACAAGAGCCCGAGCTGCTGACCGCCAGCCAGGAGCCTGGATGAAGC
TGGACACCGAGAGTCCACACTGTGTATTAGGCTGACGTGAAGTTTAAAG
ACAAGCGGGTGGCTCAGCGCTTGAAGGCCAGAACAGGCCGGGAGGGCAG
Contig 70 (1300 bp)
ATGTCAGGATAGTAACCTGGGGTGTGCTGAGTACCAATGCCAGATCCTTAA
CCACTGTGCCACAAGGGAACCTCTTACCTAGAAATCCTATACCCACTGCA
AATATATTTCAAAAAGGTAAAGTCTGAGCAGAAAAGCAAAAATGGGAT
AATTCATTTCTGGAAGACCTTCTCTTTTAAAGGAAGTTTGTGGACGTGA
TGAAGGTAGAAACTCGGAGGCACACAAAGAAAGAAAGAAAGAGACAC
TGGAAACGGAGCAATAAAGGTAAATAAAGTTTCTCTCTTCTCATTT
TTTAATTGCTCCAAAGATAGCTGACCTCTAAGTAATAAATAGTGGAAA
TGTAGCATATGCTCTAGCGTAATTTAAAGTATAACTTATAGCAATGATA
GCCCAATAAAGGAGGAATTGAGAAATACAGTTGCTGTGTTCCCATTTGT
GGCTCAGCAGTAATGAACCTGGCTAATATCCATGAGGATGCAGGTTCAAT
CCCTGGCCTCACTCAGTGGGTAAAGGATCCAGGTTGAGTGAAGTGTG
ACGTATGTCACAGAGTGGCTCGGATCTGGCATTCTGTGACTGTGGCTG
TGGTGTAGGCCAGCATCTGCACCTCCGATTTGACCCCTAGCCTGGGAACC
ACCATATGCTGCTGGTGTGGCCCTAACAGACACAAAATAAAATAAAATA
AAAGAGAGAGAGAAATATACCATTTGTAATTTCTCAGATGACACAAAGAG
CAATGTGATATTTATTTGGTATATGGTGATTGATTCAAGATGTATATCATA
ATATTGATTCAAGATGTATATATCTTTTCTAAAAAAGAGATTATACA
ATAAGGCAAGAGTGAAAAATAAGTGAATGCTAAAGAAATAGTTAATCCAA
AAGAGGCAGAAAATGGGGAAAAGACATATAACAGATGGAAACAAATAAAA
AAGAGCTAATGAGATTGTAATAATTTAATCCAAACATACAGATAATCCCAT
TAAATTTAAACACTCTCAACACATTGATTAAAGAAATTTGCAAAATGAA
TAAACAAAGCAAGACCCCACTAGATGCAGACTATGAAAAACCCACTTCAT
ATAAGACATGGGTAGGTTTAGAGCAGATGATGGGAAACCATGTCAGC
CAAACATTGTCAAAATAAAGCTGGTGTGGCTGTATTCTCAGACACA
GCAGACTTCAGAACAGAAACACTGCAAAGGATGAAAGAGATACTGCATA
ATGATAAAGGGATCAATTTCCAAGTGCAGGCTCCAACACACAGAGTTT
Contig 71 (500 bp)
ATGACCTCATACTGAATCGAGCTCGGTATCAGGGGATCTCTCAGCTGGGG
GGGAGGGCAATGGGGCATTTGTCTGAGGATGCCCGAGGACAGGCCATTG
GCTGGTTTGGTGCCCATGCCCCCCCACACCCCGGAGTGGCCCTGCTG
AGCCTGGGACCCCTCTGGGAGTTAGGGATTGGGGGTGGGAACAGGCTT
TGCAGTAATTCAGCCCCAGGGCCCTTCCCTCCCGCCCTCAGGACCCC
CAGCCCCGCCCCACAGTCTCCACTGTGACAGCCTCACCCCTTGGGTCA
AGTCTGTCTCTCCGGCCCCCGCTGGGCAGTGGAGCCAGCTAGGTGAGA
GGCACAGGCCACTAGGGCGGTGGGCACTGCTGAGGACAGAGGGGCTGGG
TGGCCTTGGACGAGGCCACGCGAGCTGAGACAGTGAAGCAGGCTCCAGG
CTTTCCAGGGAGGGTCCCTGAATGTCCACTTCTTGTGACATCGGGTGAC
Contig 72 (550 bp)
AAGTCCATTAGGGAAGGATTTGTGCAACACAGAGACAGGTGCAGGGCT
GGGCCAGCTGCTGGGCTGGGGGCTCCTCAAGGCGCCGTAAACCCCTCCC
TGCCAGCCGCTGCCGCCAAGGTCTGCTGTCCACCCCGGCCGGGCTGCTG
TGTTCCCGGCTGTGCTGCGAACCCGACTCCCGTTGACCCCTGAGCAC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TGCTGGAGGCCGGCTGCCAGGCCGGACGGGCCCTCAGGGCTGGGCTGG
CTCTTGGCTGTGTTTCATTTCTGAGCAGGTCTCTCAGTGGGGGGGGC
CTTGGGTGAAGCAGGCATGTGCACCACTGGGGCCCTGTCCCAAGTGGGCA
TCCTGGGCGCTTGTCTGGCCCCCAACCCAGGCCGTGTGCATCATAACC
TTCACCTGAGCCCCAGCCGAACCCCGACATGTGCTGGGGGACCTTGGG
CACAGGGGTGAGGGAGCAGTGGCCTTGGTGGAAAGCCAGCCTTGGCACCT
GGGGAGGGGGTGCATCTGGCATGCTCTGCTGTAACCAAGCCAGGGCAGG
Contig 73 (950 bp)
GACGTGCAGTAGCCATGACCTCTACGGCCCCACTGACCAGCCCGTGTCC
TTGTCCCGAGACCCACCCCTAAGCAATAGGATGCAGCAGAAGTGACAGAA
CGGCCCTCCGCGATGAGGTCCGAGAGGGCTCTGGCTCTGACTCAGGCCCT
CATCCCTCGCTCTCTGGAGCAGGGCCAGGTAGGGGCCCCAGAGACGC
CTAGAGGAGGTGACGGGAGCCAGCCGCCCCAGGGAAGGCCTGGGGAC
ACCAGGGAACAGAACGGCACAGGCTCTGGCACAGTCTCCAGGAGCCCC
CTGGTGGCACAGAAATCTGACCGGCCAGTGGAGGGGGCTGGGGCGGGG
CTCGGGGAGGAGGACTGGGTGAGGCCGTCTGACTCTGGCTGAGCGCCG
CATACTTGTCTGCTGCCACGATGCCGGCCAGGCCTTCCGCACGGACCC
AGGCTCACATTGCGCTACATGCCACTGTGTGGGAGTTTGGGATGGTGTG
CCCGCTGGGCCCGGGGTACAGGACAGCTTCCAGAGGAGCGGGTCCAG
AAGGCCAGGTGGAGAGGCGATAGGAGGGCTCCAGGGGGCTTCCAGGCC
ACCTGCGAGGACCTCTCTGGGGGAAGGGAGCGGAGGAGACAGCCGGGT
CCCTTAGGCCAAGGCTGAGTTGTGACCGCAGGGAGAGAGAGAAGGAGCA
CCCACAGCAGGGCAGGGGCTGCGGGAGGCTGTGCTGGGTGGCCGGGTGGT
GGGTCTGGGGGCCAGGACCGTGGGAGGCCCTCGAGGGGGAGCAGGCACGG
GAGGGGCCCTTGGACGGCAGAGTCCCTGCTCCAGCTGCCGCCCGACCCC
AGGTCCACCTTCACTTTACAGCCTGGCCCCCGGCCGTCTGACCGGCCCT
GCCCATGCAGGTGTAGCGGGCAGTGAGGGCCAGGCTCCGGCGTCCCAA
Contig 74 (450 bp)
GCAGGCTGGCAGCAGGAAATGATCCAGAAAGTGCCACCTCAGCCCCCA
GCCATCTGCCACCCACCTGGAGGCCCTCAGGGGCCGGGGCGCCGGGGGCA
GGCGCTATAAAGCCGGCCGGGCCAGCCGCCCCAGCCCTCTGGGACCA
CTCGCTTCCAGGCCCGCGGCAAGCAGGTCTGTCCCTGGGCTCCCGTC
AGCTGGGTCTGGGCTGTCTGCTGGGGCCAGGGCATCTCGGAGGAGGAC
GTGGGCTCTCTCTCGGAGCCCTTGGGGGTGAGGCTGGTGGGGGCTGCA
GGTGCCCTGGGCTGGCTCAACGCCGCCCGGTCCCGCAGGTCTCACCC
CCCGCATGGGCCCTGTGGACCGCCCTCTGCCCCAGGCTGGGCCCTTGC
TGGCCCTCTGGAGCACCCGCCCGGCCCAAGCCTTTCATGAACA
Contig 75 (1363 bp)
CCTCCAGCTGGGCCCGGCAGGGCACCGTGCCCCCTCAGGGGACACCAGGG
GGGCCACAGTGGCTCTCTGCTCCAGGCTCTGCTCCCGCTGGGGCCCC
CTGGGCCGCCGCCCATGGCCAGGGCAACTCCAGTGCGGCTGCCCGTC
TGGGCAAGAGGCCGCCAGGCCCGCGTGGTCTTAGCAGGCACTGGCGGA
TGCCGNTAACTAACCATTTCTCCGAGGAGTCCGAATCTGCTTGACCA
CGGGCCCTAAAAATCGCTCTGGCCCGCAGAGGATCCCCGAACAGCGGG
CTGCCCTCTGCTCTCTGCTGCCGGGCCGCACTCGGCAGGCACGTGCCCT
GTGCTCCCACTGTGTCAACCGTCCCGTCTGTACGATCCCCAGAGTCCCA
CGCGCGGCGAGCTCTTCCACACCCCGCACGGCCCCCGAGCTGCCTGGGC
ACCCAGATCGCCCTGACGCCCTTGTCTCTAATTCTGCTGAAATACACAT
AACGTCTCTTGAACGTTTGTCCATTTTACGGGGACAATTCTGTGGCGG
TAGGTACACTCCCTTGGGGCGCAGCCATCGCACCATCCGCTTCCAGGAG
GTCCCGTCTGCCAGATGGACACTGTCCCACTGATCCCTAATTCCCTGT
CCCCCCAGCCCTGCCCTTCTGTCTGTGGCCCTGGCGCCTCCAGGGA
GCCCCGTGCGGTGGGATCAGAAAACGTGTGTCCTTTGCGTCCGGTGTGT
GTCTCTGAGCATCCGGAGCTTGGGGTGTCTCCACGCTGCGCCTGTGTAG
GACGTCTTCCCTTTTGGGCTGCGCATGCTCCCGTGGGGCTGCCCCA
CACTGCGCGTGTTCGCTCATCCATCCACTAAGGCTGAGTTACTTTTGGCG
GTTGTGAATACTGCTGTGTGAACACGGGCGTCAAAATACCTGCTGGAGGC
CATGCTCTTAGGCCCTCTCGGGGGGCACACCCAGAGCGGATATGCTCAATA
AGGTAATTTGTGTTTAGCTTTTGGGGAACCATCAGGCTGGTCTCCAGA
GTGACGGAGCATGCGTCGCAATTCAGGAATGGTGTCTGAGGCTTTGAGG
TCTCCACCACTCGCTTCTATTTCTGTGCGTCACAGCCGTCCGAACGGC
TGGGTGGTGCCTCTGTGTGGCTTCAATGTGCTTTTCTTTCTTCTGGCTAT
GAGGTTGAGCGTTTTTATGTACTTGTGGCCATTGCGAGGGTTTTTGGG
GTTTCTTTCTTTTTTGCCTTTGGGGACGGCGCCAGAGCGTATAGAAGT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TCCCTGGCTGGGACTGAATCAGAGCTGCAGCTGCCAGCCTAGCCCCACG
CCGCAGCAACGCA
Contig 76 (500 bp)
TCATGCCATCGCCACCGCCCCACCCGACGTTTCAAACACCAGAACCA
CCCCTCGGGCGGCAGAGAGAGGACCGGAAGGAGAGACAGCCTGGTCCCAA
GGCCTCGCCCGGTCTGTGTCTCCGAGCGACATTTCTTTCTGTTCCCTC
CTCCGCGGTCCAAGTTTACCCATCAGAGGCGCATTTGTTTCATCATCTG
AAAAAAAATCTCTGTCTTAAATAAAACACAAGAAAAAGTAGCCTTCGA
AAGAAAGCAGATGAATGATATGTCTGGCGACAGTGTGGCGGCCTCTGA
GCCGTGGTGGGAGGTGGGAGCCAGCGGAGCCCTGACCGATCAGTGACC
CAGCTCTCTCTGACAGCTGGCTGCACCTGCACGCGGTGACACAGGGAC
CCAGCCTCTGCCAGCAGGTACCCCAACCCGTCCTCTCTCTGGAAGG
GGCAGCGTTGCCCTTCTGAGGGTGGGCTGCTCTGAGGGCGCTTTGGCC
Contig 77 (626 bp)
GCCATGGGCTGCGGCGGTTACGCGGCTTGGCGGCTGCCCTGGAAGTCCC
ACAGGACCAAGGGAGGGGACGTACGACAGGGGCCCCGGGACGGACGG
TGCCGCCAGCGCCCGGCCCCCGCTCCAGACAGGACGCCCGGTACCC
TTGCGGGGACAGCCAGCTCGTGGCCTCGAGCAGAAAGTGAGAGTGGG
GTGCACAGGGGCCCCCGGGGAGGAGGGGACAGCGGGGTGAGCGGG
TGGGGCGTGTCTGGGACAGCCCTGGCCTCTTGGCGCTCCTCCCG
TCTTAAACCGGCGCCAGCCTCTTGGGCTCGACCAAGGCTGTTTGGAA
AATAGGTGACCGTGGCCTGACCCGAAAGGCCAGCGGGACCCGAGTGGC
GTCCCCAATGGATCAGCAGGCGCTGGGAGCCTGCGGCCCGGGACCCG
GAGACACAGGTGGGAATGGGAGGAGGAGGAAGACGGGAGGAGAGGAG
TGAGGACACAGCAGAAACACGCCCCCTCTCTCTTCCGCTCTCGCCCTCGC
CTCCGACAGCTCCGACTCGGTGCAAGGAAAGGCCACGCCAGCCCCG
CGCCACCGGG
Contig 78 (500 bp)
TACTCGGGTTTGTACCACTGAGCCACAAAGGGAGCTCCTAAAAATAATA
ATTTCTTAAAGCCAATGACATGGAGAGCAGTTAGCGTGGAGGCTGGTGG
GTGGTGGGGCGCGGAGGCGCCCTGAAGGTCTTGTAGTGGCAGCCTTGGC
CGGGGAGGTGGGTGGGCGAGGGGTGTTGAGAAGGGGAGGGCCTCGTGG
GGGAGGAAGGAAGCCAGTGGCTCCAGTCCCTGACCTTGTGCTCTT
GAGCCTGGTTCTCCCAAAATTTGTCTGTGTCTCTTCACTTACCGGAAG
CTTGGGGCCCGTTGCCAGGGAGACAGATGGGCTGGTGACCCCAAAATGA
GCCACAGGAGGGGGGCACTGACTTAGCCAGCGGTCACATCAAGAAGC
AAACAGGCCCGCTGCTGTAAAGGCAGCTTGGGCTGGGGTCCGGGAG
CACCCCTGGGCTGGGAAAGGGGTCTCTCAGGCCCGGGGAGGATG
Contig 79 (427 bp)
TCTATTGCGCGTGGCGGAAGAGGCTAACCGTACATTGACCGGCATCTG
GCGATGTATCACTTCTCTCAACCGAAACTTCCGGCAAACTTGTCTGG
TGAAAACGTTGCGGATAGCCGAATCTTATTACCGTAATACAGTCATTG
ATGCACTGTTATGGGTGGGTGACAGGTGATGAGCAGCGACAAGCTGCGT
TCAGAACTGGCGGCAAAATACCCGTTTATCGACCCCGATAAAAAGATGAT
TCTGGTGACCGGTACAGGCGTGAGAGTTTCGGTCTGGCTTTGAAGAAA
TCTGCCACGCGTGGCAGACATCGCCACCACGACAGGACATCCAGATT
GTCTATCCGGTGCATCTCAACCCGAACGTACAGAAACCGGTCAATCGCAT
TCTGGGCACTGTGAAAAATGTCATTCT
Contig 80 (650 bp)
GGCGTTGCCGTGAGCTGTGGTGGGGTACAGATGGGGCTCAGATCCCGC
GTGGCTGTGGCTCTGGCTAGGCCGCTGGCTGACGCTCCGATTCGACCCC
TGGCCTGGGAGCCTCCATATGCTGCGGGAGCAGCCCTAAAAAAGGAGG
AAAAAAGGAAGAAAGAGAAGAAAGAAAGAAAGACAAAGTCAAAAG
GAGCTCCCTGAGCGATGTCTGTCTACGAGCAGGTCCCTGGGAGCCTGAG
GCAGGGTGAGCCTGGACCCCTGAGGGCCACTCCAGACTCAGTGCTCTCAC
TGGCCAAAGTCTTTGGGACCGGCTGGGGCGCGCGCAGGCTAAGGAGGA
GGTCAGAGGAGGGGCTTCAAGCTGCAGGGCCAGCGCAGCTCTGGGCCCG
GGCGGGGGGAGATGGCTGAGGGCTTGGCGGGCTGGAGGGTGGGGG
GCTTCTGGAGTGGGAAGACGGGAAGCCAGGTGAGAGGAGAGCGAGG
GCTGAAGCTCCTGGAAGGCGCTGGCTACCCCAAGCTGGCCCGCCCGCTG
CCACATTCAACAGCCACCCGCTGTGGTCTTGGCAGGGTCTGGCAGAA
AAGCCCCAAGGGCCCAAGCCTGGCCCTCTGGGCTTAAAGAGCCAAGCCCC
Contig 81 (550 bp)
TTAACCACGAGCAAGGCTGGGGATCGAACCTGTAACTCTGGGCTCCT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

CGTCGGATTCTGTTAACCCTGCGCCACGACGGGGACCCCCAGGGCTGGC
GTTTCCCTCTGTGTGCACACAGTGGACCTGAGCCAAACAGCAGGGCCTTC
ACCACACGGCGCAAGAGTCGGCAGCAAGAGAGCAGTGTCTCATGGCTCA
CTTTCTCCCCCTTCCCCGGAGTGGTGACAAAACCCCGCCGACCCGGACT
CGGTTAGACAAGGCGGTGCCAGTGCCCCGCTGTACCCCGCACGGCAC
GGCGCTCTCCTTTCTTCTCGGGGCTCCACCACGTGTCTCAGTTTCCGC
ATGAGAGTACCGCGCTGGCGGGGTGGTGGCTCTGGGGTGGGGGGCGGTG
AGGGCAGGGCTGGGTGGGGGAGGCAGGTCTTGGCCATTACGCGGGGGG
CAGACTCCACATCACAGCTCTCTGTGCCTTGTGGCTGCCTGACACCATG
GACTTCAAACAGGAACAGCGGTGGAGGCATTGCAGCCAGGGCCCGGTT
Contig 82 (550 bp)
TGACACCTCCAGGCAGGAGGTGCAGGCTGGGGTCCCAGGTAATGGTGTG
CTGGCCTGTGGGGCTGGGGCTCAGCTCTTAGGATGGTGGGTGGGCGCCG
ACCCAGCAAGGACAGGGTGATGGCAGGTCTGGGCTCAGCAAATGAGTGC
CCAGGTTGTGGGGTGGGCACTTGGGGCTCAGGGGAAGCTCATCAGCTTG
GAGAGGACGGGGGAGGGAGGGGGCTTGGCCAGCTGGCCAGATGCCTG
GATGTGAGCACTCACGTGCCCCGGGTCCACCTCCCTCCAGTGGCATCT
GGGCAGGAGGTCCGATGCTGTCTGGGACCCGCTGTCTGAAATGAG
GTTCACTTGGTGCTTCCCCAGAGATGCTCGGTCCGGAAGCTGACGAGGC
AGGAGTGCACAAGGGTCTGGGGAAATGGAGCAGAGTGGGCTGGGGCACA
GAGGCTGCCCCAGCCTGGGAAGATGGGAGCTTTGAGGGGTACCCCGC
CAGCTTGTGGGGCCCTGGATACCCAAAGGTGTGAAGAGGCTGAAGAGCGA
Contig 83 (984 bp)
CTGAGCCAGCTATGTAGATTAGACCCGGTCCGTCCCAAATTTCTCTCA
AAGCTGTCCCGAGATGAGAGATGAGGTTTTCGTGCTCTGTCTCTCTCG
CTTCCCCCTGGGATGTGCCCTAGGGTGGGAGAGGGTGTGTCCAGGGCTCA
GCAGGCGGTCCCCTCTTCCCGAGACGGGAGAGATCCCTCTCTCTCGGCG
CTGTCCCCACGGCCCCACAGACACCCCCCCCCGGCATGGCACCCAT
GCACCTGCCATCGTCCCCAGTAGGGGATGGGTTTGGCGAGACTGGAGATG
GCTGTAGCCAGTGAGACATGCCCTGCCACGTAGCTGACCCCTGGGTGT
GCTCTGTGAGATCTGGGGACCCACAGCACCTAGGGATCATCTTTGCCA
GCCTCTTGGGGAGCTCTCAGAAATGGGGGGCCCCAGAAGGCTGGCAAAG
GTGATGGGAGCGTGGGAAGTCTGGCGGTTGGCGGGTGGGTGGGGGCA
TGCGGGCTGGTGGGGGGTGTCTCCGGGTGGGAAGTGGTCCAGCAAGGT
TTTGGACACAAGTCAAGGAGGAAGGAGTACGAGGAGACTTGCAGAATTA
CAGGTAGAATCAGGAACCCACATCGACCCAATTGATCTATCCCCCTT
TGATTGTTTCTCCTGGGGCTTTTTCCTTTTCTTTTCTTTTCTTTT
TTAATCCCTCTTAGCTTTTACGCGCTCAACACCAATTAACGTAATC
CCACCCCAAGTAAACAGGGGGCGGTGACCCGAGGAGCAGGAGCACAG
AAGCCACCATCCGTACCTTGGCGGCACAGCCGCTGTCTGCCCTCCGC
CCATTTATCGCCCTTGAATTGATTTTGTGTTGCTGTCTCCCTGTGCTT
GGGTAGAGTGGAAAAGGGAACCTCTGTGGGGTGGCAGCCACTGGGCCCC
CCAAAGATTTCAGGGGAATGAAACGGCTGCCGCC
Contig 84 (550 bp)
TGCCCCGACAAACCTGCCCTGTTAGCCACACTCGCGACTAATAAGGCGA
GAGGTACGCGGGCAGCCCCACGGGGAGAAAGTGCTCCGTGCCCCACC
CCTGGCTCTGATGGCCAGCCTGGCACCCCAAGGTGGCTCGGCTTCTCT
ACCTCCAAGTCCAGGCGCATGTCCAAGCACCAGCAGAAGCTTCTCAGG
GTTGGTGCCTGCTAGGGCAGAAAGCAGGGGTGAGGCTCCCAAGAGGGCC
ACTGGCACCAATGCCCCAGGCAGCCCCAGCGAAGGGGACAGCCACCCC
CAGCCCGGGGACGAGGCCCTGAGGGGACATGGGGAACCCAGAGCAGGGCC
AAGGGAGCAGAGCCCTCTCTCCGGGACTTGAAATCTTCCCGGGGGGCC
CAGGGAGCTGGGTCTGCAGAGGGCACTTCAAATACGGCCACCCCCA
AATTGCCACGTGGGCCACAGAGCAAGGAGTCTGTCCAAAGTGGCCTGGC
TTCAGCGCAGGAAGTTCCCTCTCTGGGGCTCCCTCTATAGGCACAGG
Contig 85 (500 bp)
TGAGCCAGGGCCTGGCCAGCTAAGCCCTGGAGCCCTCCCGGCTGTTT
CTGCTCTCCATGCTGGCGGAGCTCGGCTTACTGAGCGGGGCGCAGGCCA
GTGTGCGTGTGAGGTGAGATTCACTCAGCTGAGGTTGAGGTGGGCAGG
GGGCGCAGACCTCAGGCCAGCTGTGGCGGCCAGGTCCCTGAAGCTCC
CCCGGCTGGCTCCCGTCCCTGCTCTGGCTTGTCTGGCCCTTGCTT
GACAAGCTTCTGTGCTCTGCTGCAGGAGAGACACTGGCTCCCCGCTC
TCGATGAGGACGGGCTTTCTGCACAAGTCTGCCCCAGAATGTTTGG
GGGCCAGCAGCTGAGCCAGCACGTCTCCCTGCCCTGGCTGGACAC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GAATCCCGGCATCGAGGCGGGAAGGGGATGGAGGGATGGGGCTACCCA
CCCCTGCTCCCCACCCAGAATAGCTGGCGGGCCCCATGGGAGGCGCCCGC
Contig 86 (913 bp)
CTGTTTTCACGTCTTCTGAGGACACACCAGAAGAGGGGCTGCAGGCGCC
CATGGTGAATCCATGTGTTCACTGCTGAGGCCCTCTGCAGACCGTCTCCCG
CAGCAGCCGCAACCGTTTCCATGCCACCAACAGCGTGCAGGCGCGACTG
TCCCCACGGCTGTGCAACTGTTTGAATCTGAGTTATATAAGCAACAGAC
GCTCCTTCAAACACACTCAGTGCACACGTGCGCACAGGCGCACAGACAC
ACACACGGAGTAATAGGCTTCCCCCCCCCTCCCTGAGCCAGAGGGGGCT
GGGGCCCTGGAGCCTGTGCTTTAGGGCCTTTTAGGAAAGCTGGTGCCCTC
CAGAGGGGCGCCCGAGCGTGGCTTCCCAAGTCCCCACCAACCCCTCGA
CAGACTCAAACTGTTGGTTCTTCTGCTGCTTTGGCCAAAGGATGGGCGCG
AGGTGGCCCTGCTGAGGTTTCAAGCCAGCGCCCGCAGGACCCCTTTCTCT
CCCGGTCCCGGCCACTTCATGGGACAGCGGGCTTCCCCACGTTGTCC
CCTGGGTGTCTGCTTTTCTGTAATGAGACGGAGGCGAGGTGCACCTGTCC
TGGGGTGAATTCCTTCTGCAGGAACCTGCTTCCCGCGCGCTGGTCTGT
CTGTCTCTCGGTTGTGGAACCTCTCGTCACCAAGAAAGGTTGGCTGTGAC
GTCCCGCTTCCCTCCGTGGCTTTTGCAGTCTGGGCTTGTGCGGGAAAC
TGCCCCAAAGAGGGGAGTGACCCCAAGAGGAGAGCTAGCTCCTGTGG
CGACAGCACCGGGGCGCCCGAGTTATGCGGGTTCACGCTCACAGTCGCA
TGACGCTGCCCTTGGACGAGGGCAGCTCAAGGGAAGCTTGTTCCTGCCA
CGAGCCACAGGCA

Contig 87 (650 bp)
TCCACACCTGTGGAGCCGCTGCCTGCTGATGCCCTCTGCCAGCTGATG
GTCAAGTGGCCAGACTTGGGGCTCAGTCCAAACAGGGGCCCCACAGGTGCT
GCACCTGGGCAAGGAGGCTGTGCGCAGGGGCTCAGGTGTCCAGGCTCG
CTGGGACCGAAGCGCACTGGGTCTGGACTCCGGGCTTCCCCAGGGGCTC
CTCGGGGCCACCTGGAAATGAAGCCCCACCTGGCTCATAGGTTCCACGTG
AGGGCCCTGAGGCCACCAAGCCACCAACCACTCAGTTAAGGAGGGGAG
CTTGGGGCTGCTAAGCTCCAAGCGGAAGCGGCGCACTCAGCACTGCTCT
CTCTGCCAGCCAGCGCCCGCTGCTGACGTCCCAACAGGCCAGGGGAC
CCTGTCCACAGATGCTGGGCGCTTCCAGTCTCTGCTCCTGGAGGCGCT
GGGCACTGTGTGGGCACACAGCCCGCACCCGCTGTAAGGAAGGGAAGG
CCCCATCCTCAAAAAGCGTGGGCGAGTGGGCGCATGATGGTCTCCGAG
GAGGTCTCTCTGGGACCCCTTGTCTCTCGGGCTCGCCAGGAGCGCGC
AGGTCTGCCCTGGATTAATCTGCCCCGATGTCATTTCAAACCTGGCTT
Contig 88 (700 bp)
TGGGGCCCTTTGGGCGGAGCGGCCAGTCTGCTGGGCGGGGAGCAGGG
GGTCTCTCTCCGAGGAGGGGGCTGGTCTCAGGGGAGGAGAGGAGGCA
GGTCTCACCTGAAAGGATCTGCTTCTCTCAGGCTCTGGGATGCTGG
GCAGAGAAACAGAAAGGAAGGCCCAACTTGTGGCTGGTGGGATGGGG
CCGGGGGTGCTTCCGGCACACCCCGCCAAACCCACCTTAGTGGCCAA
AGTGGGTGTATGATGGCCACTGACCTCACGGGGGCGCAGGAGACAACAA
AATTTACGCCACTCTTGGGGGAAGGACACTTGTGGCTGAGTCTTAGGGG
CTGAGTTTGGGGGGGACCCAGCTCTCCCCCAGTATGAGACACCCCTG
CCCACTCTCCAGCTGCTCCCCAAACCACTGCTTCTGGAGGGGATCT
CCCCGCTGCCCCGAGCGCTGTCTCTGACCATGTCCCTCCCCACCT
CCCCCTCTGAGGGCCAGGCTCCAGGGAGCAGAGCCGAGGCCACCCCTA
GACTGAGCTGGGGACCGAGACCCCAAGTCGCCACCCGGTCTCTGCGTTAG
AGAGGGGTTCCGGGGGGCACCTGGGGCGGCACTGGGGGGCGGGAAGGA
GAGCCCTGGGCGTCTTGGGAAAGGTCTGGGAGGAGGGAGGGGTTTTC
Contig 89 (1400 bp)
GCACACCCGGAACAGAGGGAGGGGCTTACCACTCTCAGGGTTTTTT
TGGGGATTCTTTGAATGCCCCATTGGTTTCAGGCTTCTGTTCTCTC
CAATCCCCCTTCTGAACCCCCCAAAATGGGTTCAAGCCCCACCCAG
CCAGAGGAAACCAATTGGGGGATTTGGGGGAGGGGGGCCAGCAAAAGCC
TTGGGCCCCAGCCCCCTGGCTTTGGGCTCTGGGCTGCCAGGTAGGGGG
AGGGACGCGGTGACCTCCGGGGGCTGGCCACGGACTCTGCCCCACCCC
CAGGGCAGACGTGCACAGGAGGGGAGAGGCTCCGAGGAATGAGGCCATCA
AAGGGACAGGTGAGGCCACGAGCGTGGGACCTGGAAGTGTTTAGGGCT
GGGGGACGAGGCTGCGGCTGCGGGCTCCGTGGTCAGGAGGCCCTCTGCC
CACTGAGCAGCTCCACCACTGGCACACGAGCTCTCTGGGGTCCGGCTG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GTCTCCGGCAGGGGTGGGCTCTGAACGTCCAGCTCCGCAGACAAATCAGA
TTCCCCGAGCCCTGAGAAAGCCCCCTCCCCAGCCCGTCTCCCCACCTG
TCGGTGGACAGAGTGACCCCTGCTGACCCCTGCCCGGGCTCCCGCAGGA
GATGTGAGAGAGTAAGAGGCGGTACAGGACGGCCGGGGCGGGCCGGGCGA
GGTGACGGTGTGTGGGTGTGAGGCTGGGCACAGGCTGGCACAGCCTCCCT
GGCCACGTCCCTTGGGCACCTCTGGGCACCTCGGTGTGCTGCCTCCTGA
AGGGATCCACCTCCAGCCACCTCCTCTCGGGCCAGCCCCACCCACCC
CCGAGCTACAGATGCTGCGATTGCCCCAAGTGTCTGGACCTGGAG
CCAGGCAGCCACCCGCTCAGCCTGGCCAGACCCAGCGTTGCCCTTCACG
CCCTCCTCCTCCCGCGGGTCTCGCGCTCGTCTCCTCAGGTGGAAAGC
CCCTTCCACCTGCGCATCTGCTGCGCCAGGATACACGGCTCAACTCA
AGGCTCACTCTCGCCCTCTCAAGGCTCTGTCCAGGCCCTCTCTGAC
CTGGCACCACTGCGGCTCTCTGGCAGCCCAAGCAACCCCTGCCACAG
TCCACGACAGTCTCTTCTGGCTCTGCCCCAGGATGCTTCTAGAAGTGG
GGGGGGGTCTTCCAGCCACGCGAGCATCCACTGGGCCCTGGGCTCCCT
CCCCAGGTGCCCTCAGAGCTTGACGCTGGTGACAGCGCTCTGCTCCGA
ACCCATGCTCCTCGCCCTTGGACCTGGTGAGATGTTGACAGGTATTG
GCTGCACCAAAAGAGTGGCCCTCAGGGTCCCCCTGCGCCCTCCATC

Contig 90 (350 bp)

GTACTGTAGGGCCTCATTGGAATAGCCTACTAGGTCACAGGTGATCCACA
CCTTAGGCCATCACAACCTCCCAGAGGTAGTGCCGCTCCTGTGCTGAAC
AAGACGGTAGTGACTGCTGTGAGAGCTCAGATCTGGTGGGTCACTGACCG
AGTGTGGAACCTGGGGGAAGGCTGTGGGTGTCCCGGCTGGGTGGCCA
TGTCATGTGCCCTTTCTATCCCTTGGACGAGGCTGGTCACTCGGCTCT
AGAGCCCCAAGCCCCAGCTGCTGTGCAACCCCCAAGCTGAGCCTCAT
CAGACCCACCCCATCGCCATGGCTACGAGGACACACCGCTCTCCAC
CCCCACGAGCGCCCACTCCCGAGGTTCCAAAGCTTGA

Contig 91 (1464 bp)

TCCAGGACCTGATGCAGCAGCCACGTCCGAGGGCCCTCCCAGAGGCC
CTTGTGACCAAGCTAGGGAAGGGGACCAGGGAGATGCTGAGAAGGGG
CCTTCCGAGGGGGCAGGTGGGACTGACTGTGACCAACACTCCCCACCC
CCTCTCCCGCTCCAGAGGGTGCCAGCCTGGAAGCTGGCAAGTCCAACTC
ACAGGTGGGCTCAGGTGGGAGGCTGGTGGCCCCACCTGGTGGGGCCC
AAGCTGCCCTTGGGCGGGTGGGGGCTGCTCCAGCAGGGTCCCATCCAG
CTTCTCCTGGGAGACTCACAGTTCTGGGAGAAGGGTCTGACTGCACC
GCAGCGCCCGCCCCCTCCCAGACTCACCAAGTTCTCTCTGATCGG
TGACTGGTCTCCGCATTGCCCAGGCTGGGCATCTGCCAGAGGATACGT
CCAAGGCAGGGCAAAGCCGGGCCGTCCCGGAGCTCCACAGGCGC
TGAGGGCTGGGCTGGATCTCGGGGGGTGGAGGGGAGGACTCAGAAGGTG
CAGCGGGTGGAGCGAGGCTGAGCCAAGGTGCACGCGAGGGCCAGAGAAG
GCCGAGCGGGCAGGAGGAGAGAGCGCCAGCTGGAGGGGGTGGGTGCC
CTGGGCAGGTCTGGGGCTCAAGAAGAAGAGAGTGTGTGTCAGGGGGCTG
TCCAAGCTGCCGGGAGGCTGCTGCCACCTCCAGGGAGCAAAGCAGGG
AGGCTGCAGCTGGCCCGGCCGGCGCTCTCAGGACACCGCTGCCCCAG
GCCTCAACGCTCCTCCCACAGCCAGGAGACCCAGGGCACCGGTCCATT
TACCGGGGCTCCGGGTCCGTTTGCTGCGCCCTGGGATGGACTGTGGGG
GCGGGCGCTGTCTGGGAGGAGGGAGGTGTCTGAGGCTGGACACCTTGA
AGGACAGTGAGAGTGACAGGTCCGTGCGCAGGAGCCTTCGGCTCTGGATT
CTGGCCCTGAGCGAGGGGCTGGCTGAAACTGGGCCGGGGCTGCCGAGG
AGAGTGTGCAGGGAGAGGAGACGGGGTTTGGCCCCGAGGTGCCGGGGTG
GTGCCCTGGAGTGCGGCTGAGCGGGAAGTGGGTGTGGCGTCTGGAGACG
GGGGTCTGGGCTTGGGATGGTGACAGACCCCCAGGTGGAGGCGGCC
GCAGAGGAGGACAGAAAGCCAGGCCCAAGCCCCAGGGCGGGAGGCTGGG
AGTCAGGAGGGACAGAGAGCCCTGGGCTCAGTGTACCGTCTCTGGCA
CCTCGCCGACGGATGCTGCGCGTGCAAGTGGTGTCCCTCACCTGAG
CCCTGAGAACCATGCAGGATGCTGGTGTACAGCAGGAGAGGGCCAGGGC
CTGGGGAGGAGTCTACTGGAAGGCCTTCTCCTCCGTTTGCAGCAGGGC
GGAATGACTGGGG

Contig 92 (694 bp)

TGGAGCCAGGGCACGGCAGAGCGTCCGAGGCCGTGCTGCTGACCCGG
GGGATGGGCGGACCTGGGGTGGGCTGTGAGCCAGGCATAGGGACCCCG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6. CONTD.

ACTTGGGCACGGCCAGGTGGGGCCGGGCAAGGGGAACAAGGACGCTGGC
CTCCAAGGGCCCCACGTGGGCACAGAGGAAGAGCCGACCCAGGTGTGGG
CGCATGSAACCCCCACTCTGGGGCCAGGAGGCCGACCTCCCAAGGGC
TGAGGCTGGGAGGGAAGAGTCCCTTTGGGGGTCACTCAGTGTCCCTTGTG
GGTGGCCCCCTGCCACTGGCGGCACCTCTGACCCCAACTCCTTGCGGGTG
GACGGTGGATGGATTTCCTGCAGCCTTCTCTTGGAAATAGTCTCTGCCAT
CCTCGGGGAAGCAGTATTGCTCTGCCCAAGTCCAGGCCCGCCCTGCAA
GGTGCTCCACCCCAATGAGCCCCGGACAGTTCGAGGGCTTCTCACGC
TACTGAGGGGTATGAACAGCTGTCCCCCTCGGAAAGTGGGGGACAGGCC
CTGCCACTCCATCCTCGGGACGCCGGTCTAGTCAGCACTTGTCTCCCTG
CCTTGTGCCCCCTGACCTTTTTTGGAGCCATCAAAACCTCAGCCTCTG
CCCCAGGAGGTCAAGCCCCCGTCCCCAGCCCCAGACCAGCA

Contig 93 (900 bp)

CCAGCCCCATCCCCGGCTGGTCCCCACACAGAGCCCCCGTTTCCC
AGGGGACAGCAGCAGCCTGCCCCAGGTCTTACATAAAGTCACCTTCTCAG
AGCTCCTGTGCGGGCTCAGGGGAATGAATCTGACCAAGCATCCATGAGGAC
ACAGGTTTGATCCAGGCCCGCTCAGCAGGTTAAGGATCTGGCGTGGC
GTGAGCTGTGGTGGAGGTGCAAGACGTGGCTCAGATCTGGTGTGGCTGT
GACTGAGGTGGCGGCCAGCAGCTGCAGCTCTGATTGGACCCCTAGCCTGG
GAACCTCCATATGCCGCGGGTGCAGCCCTGAAAGGACAAAAATAAATAA
TAAATAAAGAGAGTAAACACACCTTCTCTAGCCATAACCACTGCTCAGG
GGCGGAGGGCCAGGAAGCGGCACCCCCCGCCCAAGGTGCCCCGTGGCGCC
CGGGCAGGCGGCTCAGCCTGCTTTTGTCTGTGATGTGAGCCGCCACAGC
CCACATGGAGGGGCTGGGCTGCGCAGTAAGTCTTAACTGACGGGAGC
TTGACCCAGCAATTCAACAGCGGGCATGAGCCGGGAAGGGAAGTTATTC
GTGTGTAGCTATTAGGCGCGGAGTGAAGGTGTGCTTGGCCCTGGGCCCA
CCCTGGGGGAGGCAATCAGAGGGSTTTGAACACCTGCCATGAACACG
GGGCAAAAGCCAGCCAAAGGGGGCAGGTGCTGAGGCTGGGAACCAACCG
TGTTCTGAAATCCGGGAATCCCACTGCAGGCATGTTCAAAGGGTCAA
GACCGGGGCTCTGCTGAGAAGGACTGGCGAAGCCAACTCAAAAGCGC
ACCCCTCTGTGCAAAACCCCAACCAATGAACAAAACCTCCAGAGGGGCCA

Contig 94 (550 bp)

AGTCTGGGCTGTGTCCATGGGGTTGCCAAGGTGCCAGGCAGAGACCTTGG
GGACAAAGGTCTGTGAGCAGAAGACATGGCCACGTCCCTGCTCAGCA
GGTCCCCAGGTGGGGTCTGATGCCCTCGCTGGGGTGGGGCGGGTTGAG
GGGCCAGGCCAGACACCTTCGTCCTGCGCGAGTGTGTGCTTCTG
TTCTGGAAGGCCCCCTGCAGGTACAGGAGGCCCTGGGGCTGACGCTG
CACCTTCTGACACCTGTGGTCTTGGGGATGGGACAGGACAGGAGACCCC
GGGCTGGACCGGAGCGGGTAAGACAGAGATTGACTCTGTCTCGAGTCT
GTGACGGGCTCTCCCCGGCTTGGGCTCGTCTGCAGGGCTTTTCGGGTCA
GGGTGGCTCAAGGTGACGAAGACCTGGTCTCGGAGTCTGCAGGCCCA
AAAGTTGGAGCCCAACCCCCCGGGAGGGGGCCCAAGGACAGGAGGGCC
CAGGGAAGTCTGGGGCTGCAAGGCCGTCCGGGCTGGGAAGGCCAAGGT

Contig 95 (1200 bp)

GTTTGTCTCAGCAGGCCAAGGGCTCCGAGGCCCTAATAGCCCATATGA
CAGCGCCCGCTCCTGGCATGGGGCCCCGCTGGCATGGGGCAGGGCAGGG
CAGAGCAAGCAGCATGCAGCTTCTACCTTCTTCTGACCTCGTGGCCCT
TCCGAGGCTCAGGGGGTCCCCGAGTGGGACCCAGCCCTGGCTCTCTCT
TCCAGAGCCAGGCCCAAGGCTGGGAGTGGCCAGAGATGAGGTGCCCG
AGCAGGGCACTGCCTTGGCGTCCCATCCCTGGCGCTCAGGGCCGTACT
GTCCAAAACCAAAAGAAAGCAGTCAGCAAAACTTCTCCAGCAAGCTGGG
GTCAAAGGTGCTTCCGAGCGGTGATCAGGGTGGCCTTTGCTACTGTAC
CGTGTGCCCTGGGAGAGGCACAGGGACACAGACACACCTCCGAGAACC
TGGGGCTTCCAGGGCTCAGGCTGCTGGGCCATCCCGGGCCCTGTGGT
CCCAGGATCTGCCGGACCGTGAGCCTGCGTCCACCCCTCTGCCTGGGA
CAGGCCCCACAGAGCTCACAGCCAGGGGACCGGGGACAGGGCCCCGCTG
GGCCACCTGCCTCCAGCCTCACCCAGCTTGGGCCCAAGGCTGTGCCTGC
GACACCTGAGTCTCAGGACGGGCGCGGGACAAAGCCGCCCGGCCCTCC
CCCGCTGGGAGGAGACCCGCTGGCCCTGACGTGTGGGCTGTGAGAGC
TGAAATGTACAGCAATTAGCCCTAACGAGCCGAGGAGGGAGCGGCGG
GGAGGCCGGCGGAGGGGATCCACGAGCCGAGGGCCCGGAGCTGGCCACCC
CACCGTCCGATTCCAGGCACTCAGGATAATTGGGTGTTAGAAAGTCAGG
CGGCAGCAGAGAGCGGGCCAGGCGGGCTGTCCCCCCTCCACCCGCCCC
TTAACAGGTGCCCGAACACGCAGGTCTGGGGAGATGCTGAGTCCCAAG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GGACCCCTGGCGTGCCTCGGGGTGCTATGCTGGTTCGGACCATGGGAG
CTGCACCTGCAGCTGATTTGGCTGTGTGTGTGTGTGTGTGCACCGGTGT
CGGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTACGTGG
GGGGGGGGGACAGCCCGTGCGTGTGGTGCACAGTAGACATTTAGAAGTG
Contig 96 (600 bp)
GGGGACGAGGGCCAGCCCTCCAGCTCCACGCATACCTGCTAGGAGCTT
GCACCTTCGCGAGAGCTTTGTGGACCCCCCGGGGTGACCCTGAAGCTG
GACGCTCTCTTGGCTCTGCAGCGGCTCTACACTACCCCTCTCCAGG
GGCTCTGGGCGGCACATACACCCACCGCAGGGGAAGCAGCAAGCATCCA
CAGCTGGGCCCTTTCCCCAGCCTGTGACCGCCGCCGCCGCCCTCAC
ACCTTCTCGGGTCCAAGACCCCTCTCTGGCTGGGCCCTGGTGTGCCCTTG
CCGTGCACATCTGGGGTCCATACCCACAGGACAGGCCCACTTTCTGTG
TCCAGATGTCCCCCTACGCTAGCTGCTGTATGGCCGCCACAGCTGGCTCTGTG
CTGCCCCCTTGACCGCAAAAGACCTGGGGTCTCAGGACCCCTGCCCATAT
GACTGCTCTGGAAGACCTCAAGCTCTCTCTCACTCTGACCTTTAAG
GCTCTTGCCACGGAGAAAGCGGCTGGGGTGGGGGAGGGGTGGGTCCCA
AAGCAGCTTGACATCTCTCTGACTGGGAGCTCATTCTCCACAGCGTG
Contig 97 (1350 bp)
CCCGCCTTATTTTAAATTTCCGAAAAACAAACACACTCTCCCGTCC
CGAAATATTTTGTATAGTCTATTACAAAGAGCTTGCACCTGAAGG
CCACTGTGCTGTGCCCCGGTGTCTTGGCCAAAGGCCCTGACGGGCCAG
GGTGGCTCATTTCCCGCATCCCGCAGAGGGCCCTCATACCTCCATCGGG
GAGCCTGGCTTCGGGACCCGGGTGTGCCCTCGCTGTGGCCATGGAAGTGT
TTTCGCAAGACATAGGGGCGCAACATGGGACAGCTCGCTCTGCTCGG
TGTGGTTCCGCTGAACCTCTCAGCTGGACATCTGGGACGAGCAACCCCA
GCTTTGCTTCAGGCTCTGGTTCCAGGCTGGGCCCTCTCTGGCCCTCGCCG
CTGGGTGCCAAGCAGGCTGGTTCGGCTGTGCCCCGGGTCTATAGAGAG
CTCTGAGGGCTTCTACAGCAGCGTGGGATTCGGCGGGTGTGCCGGAGT
TGAGGCCCTCTGAGTCTCAAGCCCCACTCTTCCTCCCAACAGGCC
CCCGCCCGCGTGTGCTGTCACTGAGGCCCACTCCCTGCTCACTCGTGA
CATTTCCAGAAGCAGGGGTTCCAGGAAGCCCTGAGCTGCAGGGGACTCA
GTAGACCGCCGATCTGAATTTCCCTCTGTATCTTGGAGACAGCT
CTGGCTCAGGCTGGCTCGAGTGGCCTGAGCTGGGGACGAGACAGACTG
CAGATGGAGGTGTGAGCTGGGACGGGACGGGCCCAAGCTCGAGGAGAA
ATTGACAGTGTGAGATCAATGACGAGGACCTGGATGGGCGCCCTGGAC
AGGSCAGACTTTTCCCTTGAGCTCTGCTGCCACTCTCCCCGCCAACTCTGG
GCTCTGCTCTGGACCGAGTTGTGTGTTCCCTCTCCCGACGCGAGCCAC
CCTGCCCATTTCTGCCCCCCCAATCCAACACCTTATCGTGGGAACCACT
GGAGCTGAAAGAGGAGGCCCCCAAGGCGCCCAAGCGCTGTAATCTTG
GGGGCTCTGCCAGAGTCTCCAGGTTCTGGGACGAGGGGCGCCGTCAC
GCGGTGGCAGATGCGGCCCCCGAAGCTTGGGCTCGGAGGAGGCCCGCCCTT
ACTGACATTTCCAGGCGCGCCGCTGACAGACCGGCTGGCGTGATATTTA
GACAGGGCTATTTGGCTGACTGCTTTTGTATGACTTTGGGGCCACGAGT
TGAGCTCAGGCGAGCCCGCTTGGCCCACTTGGTCTCAGCTTGGGTTTG
ATAATATAACGGTTCAACTGAACCGCTGACGCTCGCTGGGCGCGAGGCC
Contig 98 (1354 bp)
GCTTGCAGTAGTCTACAGATTGGACGACTCATAAATGTCAAGACATCTA
AAGATTGTGCATCCAATCATTTCCCACAGGTTGTTTTTTGTATGATGT
CAAGAAGCTGACCCAAAAACTCAGCTGGAATGCAAGCTCAACTGGGAGAG
TTGAAACAATTTCTAAAGAGAGAGGAGCGTGTGGAGGACTCTTCGG
CTCTTTGGTTTTCGCTCACTTTATATTAATAGTTACTGATTTTCCATAAA
GGTCGAGTAGTGCAGACAGTGGGCGCTATGAAAGAGGAGGGGCTCAGAGAT
GGTTGGGACAGAAATGAAGAGCCAGAAACGGACCCCGCAATGTGGTCA
ATTGATTTGGCGAGGATGTGAAGAGTCAAGAGGCTCAGTGAGAGAGAGTCTTT
CAAGAAATCTCTGGTCTCGATCCACTGCTCATCCAGGCCCAAGAGTGAA
CTGGGCGCACATTTCTCAGAGTGTATACAAAACTGACTCAAAATAATCT
ACATACCTCGTGTAGGCTATGAAGCATGAAGCATCCAGAAGAAATCT
CGGTAACTCTCAGGCACTCTGGGGCTCCACCTCAGACCACTGGCTCTTG
GGGCCAGATACTACGTGTTCTCTGTGACTGTGGGACGTGCAGGCCAAA
CCCCAACAGGTGACCATCAGAAATGTTCCAGACGCTGCCAATAACTG
CCAGAGGACACAGAGCCCTCTCAGTGAAGAACACAGGGTGGGGCGAGAG
ATCTCAGACATGACAGCATTAGGCGAAACAACTGTGACACACTGGCTTTG
TTAAATTTAAACATTTTCCCTCTGAAGAGCAATGGTAAGATCATTAAGAG
CGGAAGTGGACAGCTGGGAGAAATTTGCAAACTAGATATCTCATAGATA

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

AGAAGATGCAGGAAATCCTCAAAGTTCAGTCACAAGAAACCAATTCA
AAAACAGCAGCAGACATACGATGGCAAATAACACAGAGAAAGTCAGC
ACCCGCTGTCCCTGGGGGGACGCGAGTCAAAGCCAGGAGACACAGGAT
ATGCCCACTGCCAAGGCTACGGATAACGGGAAGCAAGACACAGACAGA
AAGGATGCTTCGGTGTGGGGAGGGTGGGGTGGGGCGGGGGTCCCCC
TGGAGCAGGATGTGAAGGCACTTGGGGGGGGCTCTGCACTCCTGGGGGCC
TTTGGCACAGCGGAGGGCCCGGAAGGCTCTAGGGGACGGAGAGGGGT
GCCAGGCTTCTTACCCAGCCAGGAGACAGGCGCTGTATGAAGCT
GACGTGCAGCAGCAAGAGCAACATGCTACAGACATGTGTCTGTGTGTG
TGTG

Contig 99 (1000 bp)

GGTCTCAGGCCACGGGCGAGGGCTGAGGGTCCGAGGGGCTTGGGTG
CTGGAAAGCCTGAGTTTGAATCCAGCTCGGTTTCTTAAAGCTGTGTCTC
CAGGCCAAGGAATGGGGCTCTCTGGGAAAGGTCTGGGGTGAAGGCTGGC
GGGACCTGCCAGCCCCGGAGGGCATCTGACCAGACAGCTTCTCAAGCTCA
CAGGGCTTCATGGCAGGATGGGGAAGGCTGTGGTGGGGAGTGGGGAGCAC
TCGACACCCCTGTCCAGGCCCTTTGAGTCACGGTGGCTCTGAAAAGGGGT
TCTCTGTGTCCATGAGCAAGTCTTTGTCCGGGCGAGGATTACTAAGTCC
AAGGGTGTCTGCCCCCTCCGTGGGGCACAGAGCAGGGGGCCAGATCACGT
GGCTGTAAGTGCAGGTTGCAAGGCTGCCACCATGTCCCACTGGGTCT
CCAGTTACCTTGGGAGGTGCAGGGTGGGGTGTGGGAAACTGAGGCAGA
GAGCTGGCAAAAGAGTGGCGGCAGGGACTGGGGGCCAGACCCAGCTAA
CCGACCTCACAGGAGCTGCTTCTACTTTGCAGCTGGAGTGGGAAAA
GGTTACCCACAGCAGCGTGTGACGGCAGCGTGGTATGTCTGTGTACTTA
TGCAATATGTTTACGTGCATGCACGTGAGTGTGCTGTGTGCAATTGTGCCT
GTGTGTGTGTGATGTGTGTGTGCATCATGTGTCTATACGTGTGTGTAG
TGAATGCTTGTGATGTGTATTTGCATGTGTATCTTTGACGTGTGAGT
GAATGCATGTGTGTGAGTGGCGGCATGTGCGTGTGTGCGCATGTGTCTG
TTTATACCTGTGTGTAGTGAATGCATGTGTGTGTGTGTGTATCATGTGC
ACGTGAGAATGTGCACTCGTGCATGTTGCATGTGAGTTTCATGTACACA
TGCTTTTAACTGTGACGTGTGCACATGTCTTCTGTGTCCCTTGACAG
Contig 100 (1500 bp)

CGTATAAATATATTAATATAGAATAAAATAGATTGATAATATAGATAAAC
TAAACCCATATCAATACCGGGTGGCCCCAGCAAAAGGATACTAGCCAGTT
TATCAAGGTGCTAAGTCAGCACATAGAATGGCCACAAACGAAACCTGTA
CTGCCATATGTCCACTTAATGGAGTATGCCACTGACATCAGTGGTAGGTG
AGCTGAGTCCATCTGGGCTCCCAAGTTCGGGCCCGGCTTGCCCCAACGG
AGGTTCCCTTCCAGGGTTCCCCAAACCAACCGGGCCCCAGGTCCTCCCTG
TCTTGACTCGTTTCTGGAGTCTTCTGGGGCTCTGCAGTCTCCCTTGTGTG
GGGCTTCTGTCCCCCTGCCCTGGCCTTGGGGCTCGGCCCTGCCCTGGG
TCCCGGGCTGCGGGCTCACCTCCTTCTTCCCTGGAAGAGAGGGAGCC
AGGCTGGGCCGGGCCAGGAGGAATGCGCCTGACTCTGCTCCAGATGGAC
AGGTGGGGACATGCAGTGGCCTCGCCTTGGGCTGCTGAGCCAAGAGCAGG
ACGGGTCTTTCTGGAATGTGGGGCCAGCCAGGTTTACGCTGTGGGTGGG
CAGCCGCCAGCATCTGTAGGGCCGCTGCAGGCGCGGGGAATGACCTCGA
CTTCTGCTTGGCACCCAGCTCTGGAACAGCCCTTGCAGAGCCTCCGCC
AGAGCTGGGCCAGAGGGTCCCCGTGTGCGGGGACCCAGCAGGGCCCTC
CCTGACTCTCCAACCACCTGCCTGGGAGGAGTGGCCCCCTGGCCTCCGT
GGATCTCTGGGTGGGGCTCAGCCGGCTTGACAGCCTGGGAACAGCCAAT
GCACATCCCCAGGCTTGGCCACACCTTCCACCGGAGCGGGCGGATCTG
CATTTCGCCAGGCTCTGCGGGGAGCTCTGAGAGCCCCGGTCTCGGAGCC
CAGCCGTGGCCGTGTACGCCCTGGGGCTGTGGACAGCGTGTCTCATT
GCCCTCCGAGGTCCGGCCAGGTCCCTCCACCTGCTCGCCAGAGCC
CTCTCCCCACCAACCACACTTCTGCTGTCTGCAAGCGGGACACACACT
CCGGTTTACAGACCTTTCACGTGCGCTTCTCTGCAGAGAAATGCCTG
GAGCAGATGTTGTCCGCACGGCTGCTCCGCGAGGCTTACCGAGAGCCCC
TCACCTAAACGGCCGGGCTCAGCAGCCCGGGGCTGTCCCCACCGCCC
AGGTGGTGGGTTCTCTGTGCCAGTGTGGCATCTCTGTAAGATACCTGT
TTATCTGCTCATCTGTGTCTCCCCAGAGGTAGAGCAGGGCCCGGCA
CAGCCGTCTCGGGTGGCCACTCGCCCTTGGGGCTCAGCTTCCATGCAG
GGAGGAGCGCTGTGACACGAGAGCCCGTGTGAGTGTGCCGGGCGCC
AGGCTGCCTTAGGTACAGCCAAAGCGGCAATTAACCAACAGGCGCTCGA

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

Contig 101 (600 bp)

TCTAGAATACCTGGCCCTCCAGGGACGTGCTCTGTAGCTGCGGCTTTCAG
GGCAAAGTGTAAATTAACATCCCCAGGCTTCCCTTCCAGTTGGCACAGGG
CACCCACATGAGGAGCAGCCTCTGGGTGCCAAAGGGCCCACTGGTGCCAG
GCGCTGGGCTGAGTGCACCCCGCATGCTTCCGCGCCACTCACCTGCTGG
CCCCACCCCTGACCACAGCAGCTGTGGGAACACTAGGCTTGGCAGCCACA
CGCTGCTCTCACTGGAGGCCAGTCCAGGCAGCCTGCTTGGCTACGCTAG
CAGATGCCCGCTCGCCTCTGCCCCGCCCCAGCCATGCAGGAGCCAG
GGTGGGGCACAGGAAGGACGATTGGGGCCCAAGGTCAAGGCACATCCAGGC
CACAGCCGTGGCCACACGAAGCGGCCCTGAGGGGGCGTTGGGGGGCAGA
CCCTGCCCCCGCTGCCGCCAGCTCCAGGCATTAATTCCAGGGGACC
TGTTCACCTGGGTGGCGCCAGCCTGCCCTTGCCTTCCAAGGCCTCTA
AAATGCCCTCTTTTCGTAACCTAGGACTTACCAAGCTCAGCGAGCCCTC

Contig 102 (1867 bp)

ACTATATCGGGTGAGACTGGGACCGGTCTGCCGGGAAGCCCCACCATAA
AGGCCACGTTGGGCCACAGTCCGGGCCACGTGAGTGTGGGCGGGTCCGCG
GGTCTGCTTCTTGAACACAGGATCTTAAGAGGTACCAGCCGAGGCCAA
GTTACAGTGAGCAAGTGAGCAATGACTGAATGAGAGCGTGAGCGAATGA
GTGAGGGGTGAGTCCGTCCACACGACGCTAGGCTCAGCCAACCGCTGT
CCCCCGCTCTCACTGGTGACCAGAACGGAAAGAGTGGGAAAGAGTGGT
TGTCTCCCAACCCAGTCCCAACCCCTGGAGCCCAACCCCTCCAG
GGGTGCCGGGCTGGCCTGTGGGCCCAAGTCTGGAGGCTCTGGCACCTTC
CTCATCCGTTCTCCAGCACCCAGGTTCTGTCTGAGCCCTCTGGCCCA
CAGGCTCGGGGACAAAGAGGGCCACCTGGAGGCTCAGGGAGCCTCACCT
GCCTGTGGTCTGGCGGAGGCGGCTCTGGACATGTATAGACCGGCTG
GGCTCAGCAGCTCTGTGGAAGATGTACAGGACAGCCTGGGCCACTCTC
CCACCAGGAGAATTATTCTCGTGGGTCCCCCGGGGAAGGGATGGG
ATCCAGCGGGGACCCAGAGCGTCCAGCACAGGACCTGTCTCTCCAGC
CCCTGCCCCACAGGATGCTCACAGCTCAGCTCGAACACGACCTGTG
GACTTTGCCCTCTGAGCTGTCTTCTCAGCCGACGCGGGCTCCGCTGCA
TGGTCTGGAAGCCAGTGGGACTCGTGTGACAGGGAACAGGGGCTCTT
GGAGTGGGTGCGGGGAGCCCGAGGAGCTGCTTGGGCTTTGATGG
CTGAGTGGGTGAAGTCAAGGAGGCTCCCCAGGGCTCTCTGACCCCCC
CACCTCAAAAAATCCAGAGCATCTTTGCTTGGGTCTGGTGAAGCTCTC
TGAGGTCAAGCCCTGCGTGGTGGGCCAGTGGGCTGGAGCAGGAAGAAA
GCAGGACAGCCCCCGCCCTGGCCAGACTCCCAACCCAGCAGGAGAC
ACCTGAAACGGGATGGAACATCCTGAAAAGAGCCACCTCTCTCTCTTA
TGATCAGCTGCCGGGTCTGGGGGCCGCCAGGCCCCAGATGTCCGG
GCTGCTCCCGTCTCACATCCAGGGTTTCTGGGCCAGGACTCTGTCCCC
CAAAGCATGCAGAGGTTCCAGGCTGGGTCTTTCATGCTGCCGCTGTGCA
TGGTGGGAAGGAAGGGGACAGTCTGGAGACCCCCGCTCTCCATGGG
TGGCGCCGGGGACAAAGCCGCTGGGTCTCAGGTTTGGGTTCAAGGCA
AACGTTGATCTGACCTGGTCTGAGATGCTCGGCCGATGCTGCGTTGTC
CGCTCGCATTTTCTGTTTCTCTGGAGGCGCTGCTGCGCTCTGGCTT
CCGGCCAGCCCCACGAGGACGACGGGTGGCTGGCGGGTCTGGGGGCC
CTGCCCGCACCAAGACGTCTGGCTCAGGTTTGTCTCTGACCCATC
ACTAAGGGCCACCTCTGACCCGGAGCCCTGTCTCCGAGGTGGGAATTGG
GGGCTGTCCCTGGCGTCATAGGACCTGGTGGGGGCATCCAGGGCTGTGT
CATGCCCTCCCCAGAAGACTCTGGGGGCTGCGGGAGGGTTTCCCAAGCT
TCGGGCCAGCTGGGAGGGCGGAAGGCGCTGGAGGCCCTTGCTGTCCCA
GGAGCATGGCTTCGCTGCAGACTGGGGCCCCGACACCCAGCCACCACT
GGCGCTCTGGAAGCACT

Contig 103 (650 bp)

GTTGAGGATTCTCGGCAATTCTCTGCTACTGGCGCTCCAATCGCCTCG
ATGGGCTTCTCTCCAGATACAGCTGCAGATCTGGCGGGCACACCGTT
GAGCGTCACCTCGTAGTGACATGCACTCGTTGTCAATGGACATCCAGG
CCATGCCGACGGCATGTGGATTCTGTGCATCCGTGTGCTCCTGTCTGCTT
AGCAGAAATGGGTTCGCCGAGTCCCGAGCATCGGCCACTGGAGCGGGCAC
TAGGCGGCCACGGATCAGGCTGCTCTCATGCTCGGTGGCCACATTAACGC
CCAGTTCCGCCGATACAGGACTCGAGGACCTTGGGACCCAACTTCTCC
ACACTACCAATGGCTGGTTGAAGTTGAAGCTCGGCGTCAGATCTCCAG
CTTGGCCTTCCGCTTGCCTGCTCTCAATCAAACTGATGTTGGGCCTAT
CCGGGTGTTACGTGCTCCGTTTCGATGTTGTAGGCCAGAGATCCATCG
GTGTTCAAGTAGACCCACGCCAAACCGCTGCTTGGTCGAGGATTCCGGC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

ACTGTGCGGCGCCAGCAGGGTCTGGAAGATTTCGACGTGGCTCGGGTCA
CGATGTGTCCTGGATGCGCAGATGTGGTACTTCTGGACTCCACGGTC
Contig 104 (1630 bp)
GGTGTGTCTACTGCTGTGGCTCAGACCCCTGCTGTGGCAGGGTCCATC
CTTAGCCAGAACTTGCACATGCCACAGGTGCAGCCAAAGAAAATTCT
TACTAATAAGTTGTTCAATTTGCTTTACGTAGAGTGGCATCAACAGCAA
ATTTAAACACCATCTATCAATACATAGACCGGTTCAAAGGGAAGAAC
TTTCTATTTAGCACCTTTAATATGGCTTTGCCCGAATTTGGGACAGGG
TGCTGTGTTTTATCTCTCCCTGCAGGTGGTCCCAGATGACCAGGCCGG
TCCTGGGCGGAGGAGCCGACTGTGGATCCAGTTGCTTCCCAAGACAGG
CTGACAGGAGAGCAGCAAGGGCCACCCCAACCGAAACCAAGCCAGAAC
GAGCAGAAAGATGCCGTCTTCCAAGTGGGGGTGGGAGCTTCTCCCATC
CTCCGGAGCCGTGAGGCTGCCCTGGAGCTGGCAGGAGCCACAGAGGACCC
GGCTTTGACCGCCCTCTGGGACCCCAATCAGGACCTGACTCAGATCC
TGAGGGGCTGGACAACACCCAGGACCTGCTGCTTCCCAAGAACCGCT
GTGTCCATCAAGTCCAGATGGCACCCTGTGCCCACTGGAGCAGCACT
CCGTGGGGCAGGCTTTCCTTGGGCACCGATGCACCTTGAGGGCAGAGAC
GGGGCCCAATAAACGTTTCCAACACAGTGGGTGAGGACCCGACCGGCC
GACACGGCAGCCCGGATGCAGGACTCCGTGCTTGGCCAGCTCCCTTG
GGGTGCTCTGTCTCTCAGGGTGGATAGGCCATCATGTGGGTGGCTC
TGGGACATCCGTTCTCTGATTGGGTGAGTTTCAGCCACAGAGATATTCC
CAGGACTACAAAGCTGGGTCCCTTGGGGACCTGCTGTCAAAAAGACA
AGGCCCTGACCCCAAGTAGCAAGTTCCCCAGGGGCTCCCAAGGCTCTG
TCATCCAGACTGTGCCAGCGTGTGCCCGCCCAAGTCTGCTGACCC
GAGTCTCTGTAACATCCCGGGCCCAACCCAGCTTTACCCCAAGGCCGA
AAGCACCAGCCCCCTGCACCACAGATGAGGCCCCATGGTCCCCGACC
TAACCTCTGTCTGCAGTTGGCTTTCAGCTCGGGTGGGGCAAGGCCTGC
ATCTCAGGCTCCCGGAGAAAGTTGCTGCCCTCCACAGCAGGCCAGGGGC
TGCTGACCACCTGGGCGGGTGGATCTGCTCTAGAATGCTGCTAAGGTG
TCCTTGACAGCAGCCCGGGCGGCCCGCCCTCCAGGAAGGAAGGGGACA
TTGCCAGGACTCAGGAATGAAGCATCCAGGTTTTGAATCCCGGTCCTC
ACCACCTTCCACCTCTGACCTCAGGCACCTCGGCTTTCAGAGCTGCCCTT
TCTGACTCTGGGACACGGGCTGTGAGGCGCTCTCGGTGTGTACAGCTG
GGGGGGGCACTCTTAACGAGGGTGGGCGTGCACAGGTGACTGACCACA
GCCCTTTCCTCTCTAAAAACGCCCGCCGAGTGACCTACGGGAGGCAG
GGCCAGGAACCCCAACCAACCAATCA
Contig 105 (1820 bp)
AGTGAGCCCTGCAGGACAGTCTGCTGAGGGGTCTGGGCTCCTCAGAGG
TCTATGGCCACGGGCACTGGGAGGATAGCAGGTGGACCCCTGCATCCAGG
TCCAGGTCCAGGTCAGAGACCCCGGACAGGCTTCTATCTCAGGAG
GGGGCTCCTGGGCGAGCAGGGATGTGGCTGTGAGGCTCGTCACTCTCC
CTGTTTCTATCTCTCTCTGTATCACACACACACACACACACACACA
CACACACACAGCAGCAGCAGCAGCAGAGGGCTGACAGGGCTGCA
GACAGGGCATGGGAGGACTGCCCGCAGTGCACCCAGATGGCCACAGG
TGGGGCCCTCGTCCCACTTTTGTCTGATGCTTCCGCCAGGCTGCTGG
GAGCAAGCACTAGCTTCCAGGGCTCTGACCAGAGAGGATGGGAGGGGT
CATGGGTCAACAGGCCGCCAGGGAATGGGGAATAGGATCTGAGGGCGGGG
GCAAGGGGCCAGGCGAGGCTGCAGTGCACAGAGCTCCCTGCACCTGCAG
GACCAGCCACAGGCCAACAGCTGCAGGCAGAGCAGGGCTGCTCTGTCCC
CAGAAGCTGGCAGCAGCATGGGGTCTGACAGCCCCACCCGGGCTCCC
ACAGAGGGGCGGGTCCCCAACTCTCCCCCGTCCCACTCAGCTCA
GCATCTCCACTGCTTGAGGACGAGCCCAACACAGGGCAGACACACAT
GCACGCACACATGAATGCACCTGCAAGCAGCACTCAGCAGTAAGCAG
GTACACACATGCATGCACAAATGAACACACATGCACGCACACAGCATG
CACACAGCAGCAGCACTCAACACGATACATGCAGCAGATGCTGGTCTT
TTGTCCCGTGGAGGGGAGGATGGAGGCCAGCCCGTGGGGAGGGCATGT
GGAGTGTGGGGGCTGGCTCCAACGCCCTCGCTCAACAGGCACCAACGC
TGGACTGAGATAAGCCGGGGCGCTGGCTCCCTTGGGGCGCTCAGCAGGT
TTGACGCCACACAGGTGGCACTGCCCTTTTCAAGACGGATGTGGCC
ATGCCACCTCAGAGCTCAGCAGTCCCCCTCAGCTTTAGTGGTGTCCC
GTGCACTGTACCCGGGGCTTCTTCTTCCAGGGCCAAAGCGAGTTAG
GGGACAGTGGCGCCCATTAATTAATCACCAGGGTGTGCTCTGTGG
TGGCCTTGAGGCCAAGGTGCTCCATGGGGGCCACAGGGCTGGCAGGT
CACTTCTGAGAGCAGCCAGGGCCAGGGGGTGGCCAGGCTGGCCCGT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

CCCCATCTGGAATGAGGGCCTTGCGCAGAGGGCGTGACCCCTCTTTACA
GCAGCCCCGGGGGAGAGTGACTCTGCGTCATGGACCTGGGGGCTGACCT
GTCACGTGTCTCGCCAGTTGACCCCATCCATTTCCGGGTGGAAGGGAC
AAAGCCATCTTGGTCTCTCAGAGGACCTCGGAGCCTTTGGCCCCAGC
AGCCAGCCCCCTCCCGGGCCGCACTCTGCCCCACCAAAATCACCTGT
GCCACAGGGTCCCTTCTGGGTGTCCAGGGCAGCCAGAACTGCCCTG
CAGACACACCAGCCAGGACATGGCCGCTTGCCGGGCTGTCTGCCTG
GGGCAGCCTGACTGCCACAGACAGGCCGCTTGAGGACCATCTGCCTGAG
CCCCAAGGCACATCCACGGGGCCACACAGCCAGCGCTGTAGACGAT
GCCACTTGGGGTGGGGGAG
Contig 106 (1500 bp)
TGCCGAATAGAGGTGGAACCAAGACCCGAAAAATGTCCACATTTTCA
ATTATTAGAAATTTAGAAAAATATTTACAGGAGTTAAAGGTATTCAT
TCTGGGGGGGGTGGGCATGCCACGGCATGCAGGCAATCCCCGACCAGC
GACTGAACTCGAGCCACGGCAGTCACCATGCTGGATCCTTAACCTGCTGA
GCCCTTGGGCACTCCAGACACTCCATATTATGTAACATATTTTAAAC
CAAAAAATGACAAAGCTTTTCAAAACAAACACATTTATGGAAGAGT
GGCATTGCTTACGCCCTGGATGGTGGCTGCGGCTTGCGGGACGACGAGGG
CCCCCGGGGAGCGCTCCGCACGGCGCATCAGGACGTGGTTCAGGGGA
AGCGGGGTCACTTACGGGCTCTCGGGTGGCGTGGGTTCCTTTTCGGC
ACCACACCCGGACTCAGCACTTGGGGGTCTTAAACGTGAGAGGCACTGC
GGGCTCGAAGCCACATCACTGACCTCTCAGACTCTGTTATGTGAAAC
CCATCCGTCCACGAGACCAAGAGACAGACGAACAAACGCAAGGTGGCGC
CTAGGTGGGCACAGCATGAGGGCAGAGCGAAACCTTGCGAAATCCCCG
GCCAAGCCTGGACGTGCGCAGCTCTTACTTGACGAAACATAGGGGGATT
CAGGAACTCTTTACCGCATTTGCAATTAATTTGCTGCAAACTCAAAAT
CGTTCAAGCACAATGCTCACTGCAATGGAACCAACCGGGGTAGGTCTCG
CCCGATCAGGATGTTTCCCGTGCCCTCTGTGCGGGTCTGCCCCCTGGC
CTGGTCAGTGAGAACTGCTCCCTCCACGACGACATGAACTTCCAGGTC
CAGGCTCTCTGCTGCTCTGGACGAAACATCATCTGTGAATCTCCCGC
AGTCCCGGGGAGCCTTCCAGGGCTGGAAGGACGGCGTCCCGTTCAGG
GGCGAGGTGACGCTTCCCAAAGCTCCGCTCCTGCTAGGACGCTCAGAC
GGCATCACCCACAAACCCACGAACCTTTCCCTCGAGGGCAGAGGCTCG
CCCTTCTCCGAGAAAGCAGCCCGCACAGCTCAGCAAGGGGCCAGCTGCGT
TTGTAACCTCAAATGGCCACATAGAGTTTGCTTGGAGGCACGGGGTCTGT
CTGGGCGCCACCACTGCACACGCAGAATAGTGGGACAGCTCCGGGGT
CCAGCTTATGGAATTAATAAAGTTTACTGCTTCAACAGTACATCTTA
AGTGTAGCTGGCCCGCAGCCTGGCGTCCGCTCCGAGGCTGCCCTCTCTGC
CTGGAACCTTGTGCTGGGGGACCTCTCTCCAGCCCAACCCAGCCCGG
AGCCAGGCAACATCTTCTTGAAGACCCGCTACCTGCGCTCCCGC
TTCTCTTCTCTGGATCCAATCTCTCCGCTTCTAAGCTCTCTTGAAGGT
Contig 107 (550 bp)
ATGGCACTCGCGGTGTGACTGAGCTACCGGACGGCGGAGCAGGGCCAC
GAGGGCGACAAGCGCGGGGCTGAGAACCTGTGCGAGGGCAGGTCCCTGCG
GCTGCAGACAAGCCTCTATCGCAGGCCACAGACAGGAGCCCCGTGTGA
CCCTCAGGCTGCAGACCAAGTCAAGGCTCTGCTGGGAAACCTCGAAC
CTGATGACTGGGTGGGTGACCCAGGACCTGAATTCGGGCTCTGCAGA
ACGCTCTGAGCCTACGGGAGTGGCCACCTCTCGGTTAGGGCTGTGTCC
TTCCCTGGCTTCCAGCCTAGAGCAAAAGCATTAAATCAGAGTGTGGCCCA
GCCCGGACCGTGCAGGACCTTAGACAAAAGAGGAGGGAGAGAGATGAG
GCAGAGAGGAGAGAGACAGAGGTGGAGAGACAGATAGACAGAGACAGAG
GCAGAGAGAGAGACAGACAGACAGAGACAGAGGGCGGAGAGACAGACAG
ACAGAGGTGGAGAGACAGGCAGACAGACAGAGGCGGAGAGAGACAG
Contig 108 (900 bp)
TTTCTAAACTCTTACTAGTTCTAGTTTCTATTGTTTTCTGGGGGGT
TCTATATAACATTCGTGCTGATTGGAGATGGTTTTGTTTTCTCT
CCAACTGTATGCCATGTGTTCTTTTCTTGTCTATCACACTGGCTAG
GACTTCCAGTAAACACTAGATATGAACATGAGAGGAGAGCCAGGCTT
CTTCTCAGTCTTGGAGGAAACAGTCAGTCTTCTCATTTAGAAATGAGAG
CTTTCTTTTCTTTCTTTCTTTCTTTCTTTTCTTTTCTTTTAAAGGT
AAGGAACTTCTCTGTATTCTTATTTTTAGAGTTGTTATTTTTTTT
CTCTTTTTTAGGGCTGCACCCGAGGCATATGGAGGTCTAAGGCTGGGG
TCGAATTGGAGCTACAGTCGATGGCTACGCCACAGCAATGTGAGATCTG
AGCCACATCTGCGACCTATACCACAGCTCACAGCAATGTCAGATGGTTAA

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

CCCACTGAACAAGGCCAGGGATTGAGCCCGCATCCTCATGGATGCCAGTC
AGTTTCGTGACCGCTGAGCCATGAAGGGAACCTCCAATAATGCACCAATT
TTAAATGAAAAAGACAAAGCATCCAGCCACAGCCCTGAGTAAGGAGTTTG
GAGGCTGACCCCTGCGTGGTCTTGGGCTTGGGCTGGGCTGGTGGGCT
GGGGGGGGTGGGGGGGACCCCTGTGGACCCCTCCCTCCTCAGCCAGGCTG
CCCCCATCCCTAGCTGTGGGGGCTCGAGGAAGGCGGGTGGATGACG
GTCCCTGGGACCCCTCCTCATATGTATCTGGGTCCCTGGTCCCTCTGAGG
CCCAGGTCAAGTCATGGGAGTCAAAGGTCAGCCAGGGGGTAGCCAGAG
Contig 109 (950 bp)
TAACCCACTGACCCAGGCCAGGGATCAAACCTGCAACCTCATGCTTCCTA
GTGGTTCGGTAACCACTGCGGCCACAACGGGAACCTCTTTGCTTTGTTT
TTAGGATTTACATACACGTGATAACGTGCGGTATTTATCTTTCTCATCT
GAATTTATTCACCTAGCCCTAAGCCCTTCAGGGTCCATCCATGGTGGTGGG
AGTGGCAGGATTGCTTCTTTTTTTTTTTTTTTTTTTTGGCTGAAAATCAG
TCCAGGATTATCTTCTTTTCTGTTCATCTGTGGAGGACACAGGCTGCGT
CCGTGTGACGCTCTGCGGGGAATACGGGGCCGATCGCTTCTGAGCCAG
TGTCTCATTTTCTGGGAGAAGTACCGGAGTGGAACGGCTGGGTGCTC
CTGACGTTCTGTGCTGCAATTTTGAAGACGCTCGGAGCGCTTTCCACAG
TGGCTGCACCGACTGACATTCACCGAAGTGCACGGATTTCCTCATCTCT
TTTTCCACGTTTTCCTCCGCACTTGCTATTTTGGCTGTGGATGTCGGCC
TCTCCGTCAAGTGTGAGGGGAGTCTCCGTGCGGCCAGGCGAGGAGCGAC
CGTGAGCGTCTTTACGTTCTCTGTGGGCCACTGCGTGGCTTCTCCGG
AAAAAGGGCTGTTCAGGCTTCTTCCCATTTCTCAGTCTGATTGTTGGG
GGGTTGCTGTGAGTTGTGTGAGTTCGACGATAGGGGGGATCAACC
CTTTATCAGCTATCGGATTGGCAAGTCCGTCTCCCATGTTCCGCGGCC
GCCTTGGCACGTGTGGGCGGTCTCTTGGCTCTTCTTGGTGCAAGGC
TTCCGTCTGATGTGGGGCCATTGTTTATCTTCTTTCTTCTCACCCT
TGTTTGTATGTGATGCAAAAATCCATTGCCAGGGTCTGTGCCGAGAAC
Contig 110 (306 bp)
CGCCACCTCAATCGCCGTTTGTCTGCAACACGGTCCAGATAACCAGCG
CACCTAACAGGTGCAACACTGCCAGAACTGCAACAGCGGGCTGAAGCCG
ATGGTGTGAGCCAGTGCACCGACAACAGCGCAACAGCGTACTTGCCAG
CCATCGGACATCCCGTTAAACCGTTTGGCGTTGCCACTTCGTTACGAC
CAAAACATCGGAAGAGAGCGTAATCAGCGGCCAGACAGTCCCTGGTGG
GCAAAACACCGATACACAGCAGCATAATTGCGACATACGGGTTGGTGAA
CAGGCC
Contig 111 (800 bp)
GTTTTCCATGATGCACAGGGGGCCGGGACCGCAGCAGGGAAGGCTCCA
TCTTGGCTCTGTAAGACCTTGAACACCTCATCTCTGCTTGGCTTGGCT
GCTCTTCGGTACGCCAAGTTGCTGAGACTGATGTGGGATCAGTGGGAG
CAGGAATCTTTCTGATTCAGCCGTTTCAAAGTGTCCCAAGCAGAAAGCTGT
GATGGCAATGCCAAGGCTATCCATGGAGGTGGCTGTGCCAGGGGCCCAT
TTCTTGGGAGCCCATTCAGGAAGGAATCTTGTAGCCCGAGGCTCCAGC
AGCCAGTGCACGGCCCTGGGACTATCCGGGTAGATCAGAGGAGGAACA
GAGCTGTGGATGGTAAGCAGGTGGCCCAAGTCCAATTTATGCTGTGGTC
CCAGCAGGGTGGCCAGGAGGCCCTCGTAACCTTAAAGATCTTGGTCTG
GTCAGCTAAATTGTATGACCATTTGACTGAGCACACATCCCGTTTAAAGTA
GAATTTCAAGGATGACTAGGAGTTTGCACCTGAAGGCAGGAAGGGCAT
TCCAGGCAGAGGTACAGAGGTGAGAGGGAGGCTCTGACACTTTGGGCT
GCAGGGGTTTGTGTGACTGACGTGGCACACAGTGTATGCCAGGCCCT
GGCAGCGCTGTGTGGTGTGAGAGGAAGGGAGAGGTGAGTTGAGCCC
AAGGTCTTCCAGGCCAAAAGACTGAAGGTGACCGCGGCTGTCCGGGGCTG
GCCCGCAGACAGGAGGAGCAGGTGGGAGCTGGCTCTGTTCCGGGGAC
Contig 112 (3062 bp)
CACACCCAGGAGAGGAAAGACCCACACAGTCTGTATGACAGCTTGGCTC
GGGGCTGGAGCCCCAGTTATAAATGTCCATCACGAGCTGTGTCTGTCA
GAGCCATCAGTGGGAAGGCCAGGCCAGCTCAGCAGCCCAAAATGAAGAG
CTAGGTCTGGGATTGGGCCAAGCAGAGGGCACAGGAAGCCACATAAAC
AAGGCACCCAAACCCCTGTCTATCCACCAATGTACATTCAAGTCAACCC
CTGGTCTTCGGGGAGGTCCCTAAGATCCGGTGGCAGGGGGAGGAAAA
GTCTGACTGGATTCTTGTACAGGTGTATCAGCGAAGGCCAGGAGGAGTG
CTCGGGCACTGCCACCTCCAGGGGCATGATGGTCATGGACAGATGGCA
GTTATGGGAGAACCTCCCCCGTGGTCAGAGCTCTGGGTGCTGTACCTGG
TCATGCAATTCAGGTGGAAGGAAAGAAACATACAACCTCCACCCACAGC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

AGCTTTAGGCTGTTGGTCTAAAGGTCTGCCTCCTGGAAGAGACACGCCT
CTGTACAGCGGACACTGCTAAACCTAAAGGAAGAACTGCCACCTGGTCACG
GGACTTCCTAGGCCAACCAACCTACAGGTGACGGCCCGGAGCATCACGAG
GAGGTAGGGGACGGGAAGGGATGCATTTGCTGCTCAGCGGATCCACTGGG
GCGTTTCTGGAGCCCCACGCCACACTTTACTGCAATGCACAAGCCCC
AGGCAGCAGGACAAGTCACAGTAGCTCTGGGTTATCCAAGGAGTCAGGGA
CCTACCTGGAAGAGTCTAGAACAGGTGACAGAGGAGGAGAGGATGGTAC
CAGCAGTATAGGGAGAATCAGAAATCTGACCACCCCTGGGGGCTGACTG
ACTCCCAGACCAATGCCACACTCAGGTTCCCGCTCTGCTGCACTTCCA
GGGTGGGCCACGGGAGTTATGGGCCCCAGGTAGCATCAGAGGCTCCAG
GTACAGGCACAAGCAGCAACCAAGGAGGATCCAGGCCAGGGAGCATCC
AAGAAGCAGCAGAAGCTCCACCTTAGGTACAGTTCTGGCACCTCCAAGTT
GAGAACATGTCTTAGACAGTGCCTGACCCCAACCAATGGAGTGTCTGGG
ACTAGACTAGGCACGCCATTTTGGTCCCAGGTTGCCCATCTGTACAAAG
GGTGTGGGCCCCAGGGGGACACAATGAGCTCCCATGGGAAGGCTCTTG
CGAATCTCCTTAGAAGCAGATGTAAAGGTTGACGTCCAGCTGTGGCTGG
GATAGAAAGTGGAAAAGCACCCCTCCCGCAAGGATGAAGCAAGA
GGCACAACCAACCTGAAATTTCCCAACGCCCTGGAGATCCTTGGAGAAC
TGGGATTTCCACCTGTAGGGGCACCTGTGAGGAGAGGCTGTGTGAGCAC
CTGTGACCTGGCACAGAGGATGCCAATACTAAGAAGCATCAGCTAAAA
GTCTCCAGGAATTCCTGGAAGCTGAGGAAGGGCTCAGGAGAGGGTACAGA
AGCCCTGGGGCTATAGATATAAGGGACGTGCACACCCACTTGCAGTCCC
CATGGACCCAGGGACATTCACAGTGATGGGCAAGATTTCCCAAAATGCAC
CCCTTGTGTGTGGGCTGGTTCGGTGGGTACGACAGACCCACCAAAAGG
CACAAAGCACACACCTCAGGCTACTCTCCTCCTCCTTGTGGAAACA
TGAGCCTTGAGATGCTGGGGCACGTGAAAACACTGTACACTTAGGTCC
TGGTGAACACTGACTGGGCCAGCGGAAAGAAATCATAAGACCTACACC
CACACACAGCCTTAATTACAGCTGTGACTGGGGCTGGAGCCCCAAGAAATG
TCTACACCCATAAGACATAGCGTTAATCAGAAAACCAAGAACAGCCCCAA
CCCCACCCAGGCTGACAACTAACAGGTATGTTGAAATATCACTGGGA
ATGTTCTAGGAGTGTAGAAGACACCAACTAGGGCATGATGCAAGAT
AATACTTACGCTGGGAGTGGATGTGACACAGGGAAGCAATAAGTGAT
GGCAGAGGACTTTGATGTGATGATGGAAGCCACAAAACTTCTAGCTTA
GCTCCATTCCCAACAGATTGACTGCAACCCCATGCTAAAAACACAGCA
AAAAGAAAGAAATCCTCATTTCCAGGCATAAAATTTTCCCCAGTCTCTG
CTGTCTCCATAAGATGTCTGATTTCAACAGGAATTACGAGGCTATAAGA
AAGGCAAGAAAAAACTACACACTGTCAAGAGAAAGCCATCAGAAATAACCA
GACTCGTAGCACAGACACTGGAATTTGTCAGGATATTTTAAATAACCGTGA
CAAATACATTAAAGATTCTAATGAGAAGGGGGTAGACATGTAGATCACA
TAGATTTAGCAAGAGAGATGAACTCGAAGGAAATTAATGGGAGCCCT
AGAGTGAAAAACACTGTAGCAGAGAAGATGGGTTATCCGTAAACATGAC
ACAGCTTAGGAAAGAAATCAGTGAACCTTGAAGACAGGGCCACAGAAATAT
CCAAACTGAAATGCAAGGAGGAAAAATTAATGAAGGGGGAGAGAGAAAA
ATAAAGAACCAAGCATCCAAGAGCTGGAGGGTGACACTGAAGAAGAGAG
CATAGGCATAGCTGGAATCTCAGAAAGAGAGAAAGAAATAACCAAGATG
TAATGGATGAGAATTTACAGAAAGCGTTGTCAAGCAACCAACCATACATC
CAAGAAGCTCAGAGAACACCAAGCAAGGTAAGTACTGTAAAAAATAGCC
CGAGGTATACCTCATTACAGGCTGTGAAAATCCATGACAAAAAGAGTCTT
GAAAGTAGCCAGAAACAGAAGGCGTGTTCATTAGAGGGGAAAGACACC
ATTGTTGCCAGAAACCAATAAACACAGGCTGAAAGGGTAAAACTTTTTT
TTTTTTTTTTTTTTTTTGGCCATGCCTGTGGCATGTGAGGTTTCCCGA
TCAGGGATCAAC
Contig 113 (1300 bp)
AAACGGATAAATACAGGTGACCCACAGGCAGAGCTGAAGTACAAACAGT
TCACAACGGCACCCAAAAAATACCGAAGGCTCAAGGGTAAATCTGACCCC
AGATGAAAGGCCCTTCTCACGGAAATGGCAAGTGGCGCTGAGAGGCATG
AGAGGTTGGAATAGATGGAGGGCTCCGCCGTTTTCCCGGTTCCGAGGATT
CAGTGACGTACAGAGCCCAATTCCTCTGAAACGCCCTCTAGGTTTCACTG
CAGCCAGACCCACTGGCAGCCGCCCTCGCTGCAGAGACAGCCAGCTGG
GTCTTGAGGTTCTTACAGCGAAGCAAGGGTCTAGAAAAGCAGAGCTCT
CTGGAAAGGGAGAGCAGCCGATGGATTGGCATACGGCGCAGGAGATTC
CTCGGACAGTGGCACCAGGAGAGGGGTGGACAGAGACTGGTGCAACCGAG
CGGGCCAGGAATAAGTCCACACCCACACGTACCATCTCGTTGTTATTT
ATTTTTTCTTTTTCAGGGCCACTCTGGGCATGTGAGGCTCCCCAGCC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

AGGAGTCGAATCGGAGCTGCAGCTACAAGCCTACCCACAGCCACAGCGA
CACAGGATCTGAGCCATGTCTGCAGCCTACACCACAGCTCCCGGCAATAT
TGGATCCTTAACCCACTGAGCAAGGCCAGGACTGAACCCACGTGCTCAT
GGATACTAGTTGGGTTTGTACCAGTCACTGAGTCAAGTGGGAACTCCTTTAA
TTTTAATTTTGAAGGTTCAAGACTCTTAATTTTGTAGTGAGGTATAGA
TTATATTACGCACCATTTCTTTCTGACTTCGGTGCACGGCTTTTCAACAA
ATGGGTGCTGGACCTGCTGGGTGCCTTCTCAATGAACCAAGCCCTC
CCTCGGCCGTATGCAAAATTTAACTCGAGGGGCTCATAGACATAAACGT
AAACTCTAAAGCTATAAAATTTCCAGAGAAAACGTAAGGAAAACCTTTG
GGTCTTGGGCAAGATTCTTACCCATGACAGCAAAATTACAATCTACA
GAGAACTGGTGGCCTTTATCGGCATTAAACACCTGCCCTTTGAATGA
TGCTGTCGCAAAACCGAATGACAGCAAAACGATGCAACTAGCAGGTCT
CACACTCACTGACCCAGTCAAGAAAGGGAAGACACGCCACGTGACATCC
CTTAGATGCAGAAATGTAACACCGGCCCGTGAACCGACCTCAAGAGAG
AGACAGACCTACAGACGACGCAAAATTTGGGTTGCCGAGGGGATGCCG
Contig 114 (3000 bp)
TGTGAGACCCCTTGGCGGCCAGGACCCCAAGTGACCGAAGGCTCA
GGGCCCCAGCGCCCATCCCTCTTTCCGACACAGGATTTTTC
CACCAAGCTCTGTCCCTTGGTCACTCTCACTTGAAGCAGCTCAGGCT
CTCCCGTGGCTGTATCCAGCAGCGTGACCTTCTTGGTGTCAACCC
AGGACCCACAGCTGGCCAGCCAGCCTTCCAGAGCACCCCGCCATCC
TCAGAGTCCAGAGGAAAGGCCCTTGAACCCAGAAACCAACGAGA
GACTCTGGGACGCCAGCAAGACGTACACTGACTCCACCTGCTTCAGGC
ACGGAGGCGAGGGTGGGTTATGAGCGACCCGTGAAGGGCTCTTGTG
CATCGAGGGGCTTCCAGGGCTCTAGACGGGATGAGTGTGGCAACATG
TCGCGCATTACAAAAGACCTGCAGTGTCTGGGATGGGTCCCGCGG
TAGAAAAGCAAGGATTCCAGCCAGTCAAGTAGGAGCGGCTCGGAGG
CTGCAGAGGCGCGGGGGCTGACCACTCGGCAAGCCCGTGTGG
AGGGGACGCCCGGCCGCTGACCGGCTGCGCTCCGATAAGCTCTTA
AGAGCCCGCTGCCCATGACGCGCTGCACACTCGCTGCCCGAGG
TCCTTCAGCAGACCTTGTGGGACGAGGACCTGGCAGGGGTGTGGCT
TGGGGAAGGGGTCTGTCCAGGAACCTGTCTGGATTGGGGTGGG
GTGGATATCCCGTCCCAACCTACAGAGGAGGGGCTTAAAGAGCCCC
TTTGTGTGAGGGGCCAGCAATCTTTGGCTTTTCTTGGCCACTTGGGA
GCTTGACGTCTGGTCACTGACTGGGAGCCAGGGCCAGAGGGGGAGCG
GGCTGAGGAGGTTACGGCCAACTCTCTCGGCCACTCCCGAGGTCG
GGCAGCTACGGGGCCCCAGAGACACAAGCCCCAGGGGCTCTCCCCC
GGCCCTGCCAGATCACAGGAGACCAAGCAGCTCTGCTCCCCGTG
CCTGAGAAATGCCCATCTGGGTACCAAAATCACCTCCAGAGGTAGA
GTGGGGGGCCAGGACAGGGGGACCCAGTTACAGAGCCCGAGGAGGCT
TCCAGGGGGAGGGGACTCCGTTTGGGGCAGAGCGGAGGAGAGGGG
CTGATGGATTCTCCCCGTTTCAAGGATGCTGGCTGCTGGCTCCAGGA
GGCGGCGGTGCATCTGATCTGATTAAGGCTGCACTCCAGCTGGGCG
GCACAGCTTGGGGCTCGGCGGCGAGGGAAGAGGCGTGTGCCCCAGC
CGGTCAGGCTCGCTTCTCTTCTTCTCTCCATTAAAGTGTGAGAAC
CATTTATTGATTTTAAATCAGGACGTGCTGTCCGTGACACAGCAAGT
GAACAAAATCAGAGCAAGAGAGGCGAGGCTGAAGCCCCAGAGGGCGGC
GCCTCAATCCGGGTGTGCCCCGGGGCTCAAGCCCCCTTCTTCTGG
GCTCTGGGCTAGTGGCCAGGCGAATGCACCTGGCGTCATCTGGGA
GGCTTGGCCATCGCTGGCTTCTGTCTCATGACGACCGTCTGTTCCATATC
TACGGAACAGCTTCGCATTAAACAGGACAGGGAGGCGGTTGTTCTCTT
TATCTGCCACCATCGGCGCTGGGGCCAGTGGAGCCAGCGGCTGACT
TCCCGCTCGCAGCAGGGCACTGATTGCAGGAACGAGGACATCCAGCCCC
CGCTCTCAATGCCCGGGTGTGAGAGCATTTCGCCAAACGGCTTGGG
TGGGACAAGGATGGAGCTGTGCGCCAGGGGCTGGCTGGGGCAGAGGG
GGCTGCCCGTGTCTGCCGTGGCTCCAGCACCTCGGCTGCCAGGCTG
CTCTGGAGAGGTGCCCGGGGCGAGGGCCAGGGGCACTGTTCTGCC
CACGTCTCTGTCTGTGAAAGTTCCACAGACGCGTGTATACCTG
GGAGTCAGGAGGATGGGGATAGTTGGGGCTTGACGTCTGTTCTGAAAA
AACACCGTTTCCCTGAAATATATATGTATTAAATTTTCTGCAAGATAAA
ACTGTGTATAGTTTCTGTGATGAGAAACGCATCCATCTTCTTAGAAA
GCCTGAAGAGGTACAGGAGCCTATAAGGACAGATGACAGATGCCTCTA
ACGCACACCAATGTGCGGTGGCCCCAGGGGACCGCATAGACGGGGCGG
CTCCAGATGGCCACCGTGTGCGAGGACACGGTTCAGGTTGCAGAGTAT

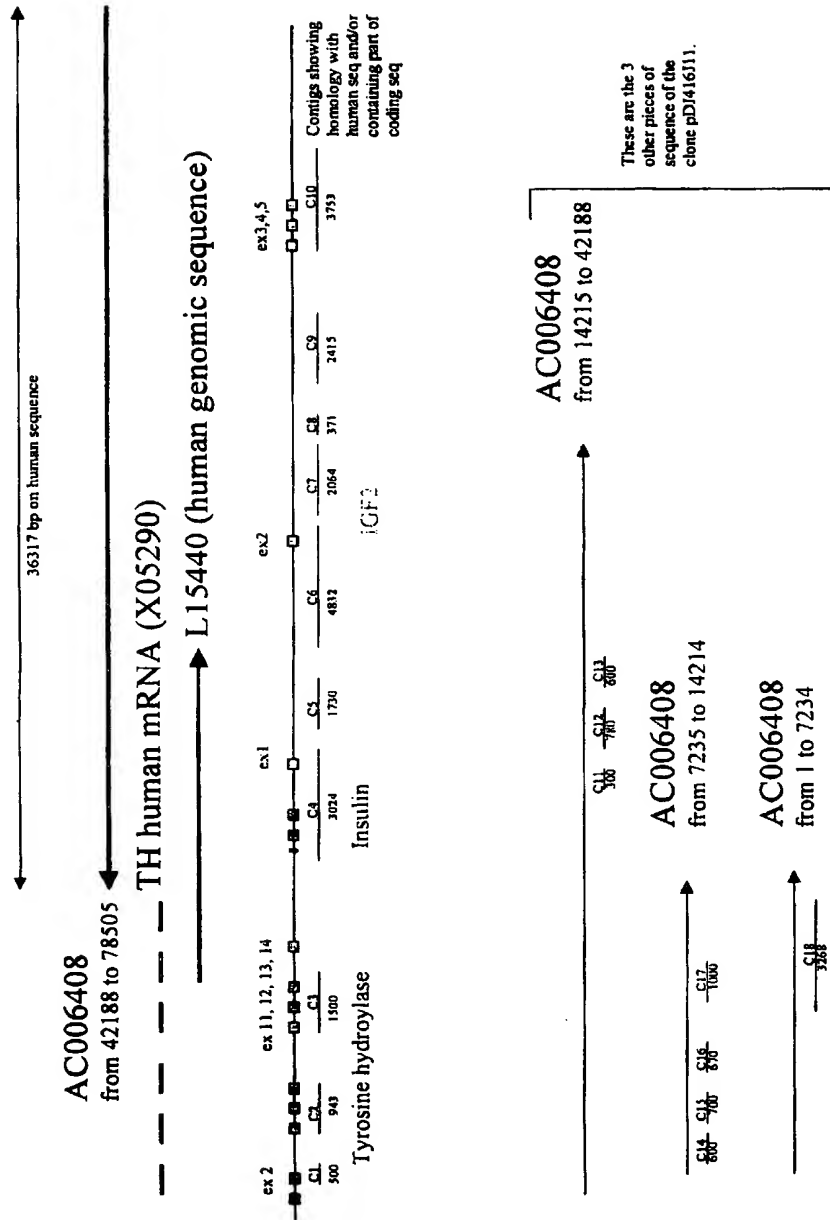
SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TCCTGGGGGGGGGGCTCAGCGGTCCCATTTCCCTCCCTTCCTTCC
TTCATTTCTTCTTCTTCTTCTTCTTGTGGTTTAGGGCCGCACCCG
CGGCGTGTGGAGGTTCCAGCCTAGGGGTCTAATCAGAGCTACAGCTGCC
GGCTCCACACAGCTCAGGCAACGCCGATCCTTAACCCACGGAGCGA
GACCAGGGATGGAACCTGGGACCTCATGGATCTTAGTTGGGTTTGTTC
GCTGAGCCACACAGGGAACCTCAGCCATTCCCATTTCTTGCTCAGTTCC
AAGAATTCCAATTCTTATTCCTGTTCTTTAAGGCCAGAGGCGACAGCCAC
GCCAGTCCCAGAGCAGGGCTCAAGGATGCTGCTGTTGACTGTGTCCGT
GGCGGGGGGAGTTGATAAGAACCCCAACACAGGGTGGTGGCCAGCAAC
GGGGAGGGAGGAGGGGGCTGGTGGCGAAAAGTCCCTGAACCCCATGG
GCTGCCCTCCAGGCTGGGGCAGACCCGAGCCCATGGCCGAGGAG
AAACGGTCCCAGCCAGGCTGGGCTCCCGCACCCCTGCCCTGACCCGCG
Contig 115 (1895 bp)
TCATGGAAGCCCTTATCACAACCTCGGATCCAAAACCCACTGGCGGAGTC
CAGGGATAGAATCGCATCCCCACAGACCTATGTTGGGCTCTTAACAG
CTGAGCCACATGGAACCTGGTAATCTATTTTAGATGTTCTAGGGTTT
TTGGCTTGCCTGTACGTGGGGACGCTGCTGGGCCAGGGATCAAAACCCG
GCCAGCTGTGACCAAGCAGAGCAGTGACAGCACCGGATCCTTAAGCA
CGAGCCAGCAGGAGCCCTGTGTTTAGATTTTGTGAGGATACTGCGT
GGGATTCAGGATATTCATTTGGGGCTGTGGAATTGCCCGTGCCTGTTT
AAGCAAGAGAGAAATCCCTTCACTCTGTGTAACCTGAGGGAAATCCTTAG
TCTCTTGAACCATTTGCGTGTGTTAAGAGTGGTAACCTGCCACCAATA
ATGCCAGACACAGCGCTTCTGAGATCCGCTTTTGTGCAAAATATCTGG
TTTGAATGCTTTGATCGCCCGACACAGACAGGGTGGCGGACGCCGCCG
GGGACCCGACGTGACCATCGTGTCTGTATCCGCCCTTCTCCGGCAGC
CGCCCTCGGTTGCCTCTGGCTGCTTTAGTGGAGGAATGAAGCTCCGC
CACCCAGACCCGAGACCGCAGGACCCACAATGCTTCAACACCTGCCCT
CTGACTTTTACAGGTCAAGTTCCCAACGCCGAATTTGCACCGATTGGCT
ACAGAGAGCACGGTGGCGCAAGCCTCCACTTGGAGTTTATAAGGTCCTC
CTCCAGCTCGCAATGAAAATGAGCTGTGATAAGGCAAGACAAAATTAG
TATGAAATCCAGATGCTTCACTACAATACAATGACCGCGGATTGGGT
CTGAGCGACTGAAATCAAGGTGGGCTTCCGGAGGGAGGCTGTTAGAGGAA
AGGCATTACGGAGGCTCAGGTCCGAGAGGCTTCCACACCCCTAAGAGGG
CTGAGACGGCAAGTAGGACCAAGCCCGCAGTCGGGAGAGCTGGGCAGG
AAGGAAGTCTGAGGTCAACCCACCTGGGGAGGAAGTGCCTAGAGAAGCG
GGGGCGGGAAGCAGGGGATGCCAGTCCCAAGACAGGACAGGGCGGAAA
GGGCTCTCTGACGGCCCTCAATGCTGCCACAGTGTCTCGTAAGAGGAG
GCAGAGAGAATTGACACCGGGGAGACACGGGACACGGAGGTGGAGACC
GGGCTGCCCGCGGTGCCAGTTGCTCCCGAAGCCGCCCTCCCCAGAG
CCTTTGGGAAGAGGCCCAACCTGCAGTTCTGCTACTCGGGACAGGGAC
AGGGACAGCCCTTGGAGCCGCTTTAGGGGCAGCATCCCCAGAACCT
TCCTTAACAGACCATCTGGAGAGAGATGGGTCTGGGCTGCAGCTCCTGGA
ACTGTTTTGCCACCCGGCGAGCACCAGTGGGTGCCAGCCTGGGCTGCC
AGCCTCAGGGCCGGGAGGGCTGAGGGCACTGGGCGCCGCTCTGGGACT
CCCTGCCTCCTGCCCGTGACGACAGCCACCTCCAGCATCTGCTTCCT
GCCACCCACATCCCCAGGACCGTCAGCCAGGCATGCCCTGGCGTCGGC
CACTCACACCACAGGCCAGGAACCAAGGGGCAACACAGAAGGGCAGTT
GCCATCTGCAGATGGAATGGACAACTGGGTCCGTGATGATGGCAGGCT
CTGGGCGCCCGGCTGGCAGGGAGCCAGGACTGTGCGGCATCACAGGA
AGGGCATGACGGGTGAAGCAAGAGTGGAAACCTCTGCCACCCGCTGG
GCGCACATACCGGCCACCTGCAGCCCAACCCCATTTGTTTGCT

SUBSTITUTE SHEET (RULE 26)

FIGURE 7



SUBSTITUTE SHEET (RULE 26)

FIGURE 8

Contig 1 (1040 bp)

GC GCGCCGGATCCTTAATTAACTGAGAGATCTGCGGCCGCGGCCAGGGTCTGCTTCTG
GCCAAGTGTGGGGCTCTGCTCCATCTGGCTCGGAGGTCCACCATGGCAAAGCTGGGG
TCCTCCCACTGAATATTGGGGGTCCACTCGTGCCAAAGGCTGGGTGTCCAGTGTGCCAA
CGGTACATGGAAGCAATGTCTTCCCAAGGACCGTCCAAAGTGTGGTCAGGCTGGACAGC
TGTGAGTCCCTTCGGGACTAGACTTGGTGGCCGAAACCTAGGGACCGTCCCGAGGGCCC
CCACGAGGCCAGGTGTTTGGCCGAGGACAGAACGGCCAAAGGTGGCCGAGGGTCTTTT
TGTTTGTCTTTCTTCTTCTTCTTCTTCTTGGCCGAGGGTCTTAAAGCGCTCTCTCTG
CTCTTGTCTCCGATCCTGAGCGGGCAGTGTCTGCTGGTGGGTGCTGGCCAGCCGACG
CAGGGCTGAGAGAGCCCGCTTGTCACTAGGGCGCGCGGTGAGCCAGCGGCATGCCG
TGTCCAGACCTTGGATGGGGCAGCGAGGGGACTGGGTGCCAGCCCGCTGGGAAGCC
CGCCCTGTGGAAGCCGCTGTGCTCGCCACAACAAGCACCTCGACTAGCTGGTGAATCAG
CGCCCGTTCGCCCCGCTAATCCAGGCGCTTCTGCCCAACCTGAGCCCTGACCCACACC
CCTTGGCAGCGCTCCGTGGACCTGGGGCGATGAGGTGAACCGTGGGCTGGCCATCGTG
GTGGCAGCGGTGGCACACCCGTGCGCTGTGCGCCCCCTCCATCCAGGAGCAGAGTGC
GCACCCAGTGGGGGCTGGGCAGGGAGCCGCTCCACCTCCGCCCTGAGGGGACGGGACTC
TTTCGACCCGGAGTGGGAAGGGACATATGCGGACGATGCCAGACCTGTCTGTGGGGGA
GGGGGAGAAGGCCCTCTTTGGAGAATTCCAGGACGGGTGAGGAACGTGTCTGGACCGGC
CGGTCGGAGGTGGGCCTTC

Contig 2 (9234 bp)

GGCAACCAGGGGAAGATGGGGAAGCGGGTGCACGGCGCTTTCGCGGGCCAAAGGACCAC
CTTGGAAATCTGGAGCCTGGCAGGAGCGGGCAGGGTTGAGGGGCTGGCTTGGGCAGGGC
TGGCTGGCACCTGGGAGCCTGGCGGGGTGAGGTCCGGGCTCCAGGTCCCTATAGGCA
GGCCACATCCGCACTGGGGGTGACAGGCCGAGCTGGGGTGGCGAGGGGAAGCGGGGA
GCCAGGCATTCATCCCGGTCAATTTTGGTTTCACTGTGCGCGCTGTGCTCAGGGGA
GTTGAGAGAGGTTTCGCCCCGGGGCTGGGGCAGCGAGGTGTAGCTGGCAGCTGTGGGC
AGGTGAGGACAGCCGCTTGC CGGGCCAGGTGAGTCCCTTCCCTCCCGAGGCTTGTTC
TCTGGCCTCTGCACTCCGAGGTTCTGGGGAGCGAGGGCCGGCGAGGGCAAGCGGCTGAC
CCCCGGCAGAGTGGCGGGGACACAGCCAAAGCGGGCAGAACAGGTGACACGTCTCAG
GGGGAGCTGGGACCGGGCGGGCTGGGGGGCGGGGCGTCCAGGTGGAAAGACATCT
CAAGCGAGTCTGGTGGGAGACGAGGACGGCTGCCAGGAGGAGGACGCAACAGCGG
GGGGCATTCAGGCCCGGGTCCGACAGGACCCGTCGGGGTGTGAGGACAGTGGGGTCCC
CAGCCGCACTTCACCCACTGCAATTCATTAGTAGAGGTACAGGAGCGGCTCTGGCCG
GGCCTCTTGAGGCTGAGCTGGAGCCTCGAGGGCGGAGAAATGGGAAGAGGTGCAGTG
TGCCAGACAGAGCTCACCTGGAGGGAGCACGGCCGTGGGACGGGCCCCAGAGCAATTC
GGCAGCAGGGAGGCTGGCGGGGGCCAGGCTGGGAGCTGGCTTCCACGCACTGCGG
CCCAGGGGCTGGCGGGCAGGGCCCCGGTGTCTTGGTGGCACTGTGCGCCCTCGCGGC
TGGCCCCCTGGGACTGGCAGGCGAGCAGGACAGCACCGGGGAGTCAAGGGCACTGACG
AGACCAGACTAGGCGAGGCGGGTGGGGTGGAAATGGATGTGACCTCTGGGGGAGGGAGGT
GGGGACGCAAGCAGGGGCGAGGCGCGGAGCCTGGCGCGAGCGAGGCCAAGGCGGGCT
CTGGGGGTGACAACTGAGCACATATGGGTACCTTTGGCTCGCACCGGAGACAGGTGAGT
GTCTGGCCCCGGCTGCGGCCCTCCCGCCCCGCACTGCTCTGCCCCCTCCCTCGACC
AGGGCCCTCTGCTTCCCCACAGCCTCTGCTCCAGTGGGGTGGACACACTGCCAGCACA
CAGGCCGAGCGCAGGATGTGCTTGGAGGGACATGACACAGTCCCGTCTACGGAGAGGG
ACAGAGCTGACGCGGTCCGGCTTCTGCTGAGGCGAGGTCCAGGCTTGGCCCCAGGC
CAGCCGCCCCACCCCGCCCTCATGGGCTCTTCTGTCCCGCAGAACACTCTCGGCTG
GCCCCGCGGGGAGCTGCCACACCCAGGCTGTGCTTCTGCTTCTGCTGAAGGAGCAGT
GCATGACTGCTGCTCTTGGACCCCGAACCCTCAACGACAAAGGTGAGGACAGTCCCGC
CTGCCCCACACGTGGAAGGGGCGTGGCGAGAGCCGGCGCTACAGGTGCCCCCTCCC
CCTGCAGAGATGGTGTACCCAGCTCATGCTTGGGCTTGGACCCGAGCTTCTCAAGTC
CTCTAGTCTGACTCAAGAAATATGCTGCATTCTGGAGCCACTACACTACTTGACTCAGG

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[illegible]

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FIGURE 8, CONTD.

AAGAGCAACGCTCTGAGCTAGCTCCACGCGTGGGTCCATCTCGGCCAGGTTTAAAGAGCC
ACTTTCAGGCAGGGATTGCACAGGAGGCAGGGTGGGAAGTGGCTCTGCTCAGACCCCTGA
ACAGGCTCTGGAGATTCTCCAAGGGCACAAAAGAACGACGATGCCCTGGGGTCAAGCA
CAATGCTCCCTGAGAAATCTTGGCACACAGGGCTGGGCTGGAGGTGGCCCTCGCCCC
ACCCAGCCTCTGGAGGACAAACGTCGCCCTGCTCCAGAGCTGGGGGGCCACACAGT
GGGGCACAGGGAGCATGGGCCGATTCCAGGCTGGGCTCCCTCTCGTCTCAGGATCTC
CCCGTCTTGTCTCAACAAGCCCTGACTTGGAGGCCAGGGTGAACCCCTAAAGGGG
GAACAGAAGGTTCTAGAAGGAGCGTGGCCAGCTTGGCTTCCCTAGGGCTGTGGTGACCA
CACTGGGCCACGGCCAGGCCACCCACCCGCTCTTCCCTTGGCCCTCCCTTCCC
CGCAGCTCTCCCTGGCTGCACCTGGTGACACGGCTGGCTCCAGCCAGGGCTGAGGGGG
ACCCAGGGGGCCCTTCTGGAAGCCACCTGCAGGCGGGTGTGGGAAGGGGCTGTC
TCCTCGCCGGCCACCCGCGCCGGGGCTTCTGGAAGCGGTCACTGGATATTTGTT
CCTTGTAGGCCGAGCTTGCTAAAGCAGACACTGAGCTCCTTGTCTCCGGAGCAGG
CGCTCCATCACCAGAACCTTGGCCGACACAGGGGGAGCCGGGCTGGGGAGCAGCG
CGGGCTGGGGCGGACCAAGCATACGGCGCCGAGCGAGGGCCCGCCGCTTC
TGCAGGCCGCCACGTCGCCAGGCCAGCGGTGCCATCTGCAGGCTGGGAGGAGGC
TGTGGCGCAGAGCTGAGAAGGGGGCAGAGCACTGGGGGGGACAGCCGTGTCCACA
CTTTGAGAAACCTTGGCCGGCTGGATGTCTTGTGGAGAGCTGGGGAGGGGACAGG
GCAGGAAGCCGGTCCCCCGAGCGGGTAGGAAGAGGCTCGGCCCTGGGAGGAGGAGGA
GGGAGGGCAGTGAGATGGAAGAGCACAGGGGGCTCAGGCTTCTTCTGGAACAAGGA
CTAGAAGGAGGAGGGCGGGCAGCTGCTTGGGATGCTTGAACAGGCCCGCCAGTGCTG
ACAGGGACGTGACTGGGGCGCGTCCCGGCCAGGCCGGCTGGGAGGGCGCTGGTGG
GTACGGCCACTCAGAGCCCTGGCAGCAGGGGGCTGGGCAGGCTGACAGACAGAGCTC
AGGACACAGATGGGGGGCAGGACTGAGTGGGGCACACAGATGCTCCAGGAGGTGGCCA
AGGAGTGGCTTGGGATCCAGGATGGCCCTGGTCCAGAAGATGCGGCAGGCCAAGGGA
CCAGGCCAGGGCGCGAGGGGGCCACAATCTGAGCAGGGCTCAGGCCAGGGCAGAGGCC
CTCCACCCAGCCCTCCCTGGGCCGCTCTCC
GTGCAGGCACTGGGCTCAGATGGGGCAGACATGAGACAGGTCCAGGGAGAAGCGGGCC
CCTTGGCTTCACTCAGGTGGCTTTCAGACCCGCGCCCTGCGTGGCAAGGCCACAGCGC
TCAGAGCACACAGACCCACACGGGCTCCCGAGGTGGGGCTGACATCAGCCCTG
TGTCACAGCAGGAGCTGGCAGCTCCCGACCGGGCTTAGGGAGCGGGGACCTGAGCCA
CTGTGCCACCGCCACCCACCGTGGCCACACGAGGGCCCGCTGCTCTGGGTCTGGGG
CCAAGGCCCCCGAGGGCGCTGGCACTGTCTGCCCTCCCGTGGCTCTCCGCTCCAGTG
TCCCCCGCAGAGAGCATGGGGCCACAGGCTGAATGCCACCTCTTCTCTCTGAGG
GGGCTTGAAGTTTGGGGTTACAGAGTGGCTCCGGGGTGGGTCCAGGCCACCGAGG
CAAAGCGGACCCAGGAGTCCCGGGAATGTGGGACAGCCCGCTGAGATCTCGGGGG
GGCCAGCTCTGGTTGACCTCCATCTGGGGCTGTGGGCTTGGTCACTGGGGAGGCTC
ATGACACCCAGCCACAGCTGGTGACAGCCCTGGAGCTGCCGCTCAGGGCTGGCTGC
CCCTGCAGCTTGAACCCCTGTTCTCTGGGAGTGGGGCGCAGGGGGCGCGGGCAGGG
TGAGAGACGAGAGCTCTTCTCCAGAACTCTGCTGCGATGAGGACCCAGCAGGGGCC
TCTCTCACCAGAGGGCTCTGCCGGCTGCAGGGCCCGAGAGGGCCAGAGGCTGGAGG
CGGGGCTTGGGAAGAGGCGGACTTCCAGAAACAGCTGCCGCTCCGACACCCAGC
GCCACTTGGGAGGGGGCGCGCCCGTGGCCCGCCGGGTCCACTGCTGGGGCGGCCA
CAATAAGTTTGTCCCTGCTGGTTACTGTCCGTGCTGAGAGGTTTCTGGAGCTGGCCA
CAATGGGCGTCAGGATGCGGCTGGGAGGAGCCTCGCGAGTCAGAGTGTGCTGGTCTCGG
ACAGGCCCGCGCGCCCGCAGCCGCTGCTGTGGACAGATGGTGGGTGGGTGGTGTGCG
GAGGGGTTGGAGAGGTTGGGCGGGACGAGGGGCTTCTGCACTGTGCCAGGGAAGCG
GGGACCAAGGAGGGGACAGCCCGCTCACCAGGAGGCTCTGCTCTCTCACCCTCCGG
GACAGGTGAGCTCCCGGAGCCGCTTCTGGGACAGGACCCAGGGCAGGCCAGGGCC
CCCCCACCCCGTGGTCCCTCCGTCCACGGCCGGCTGGGGGGCACGGGCCAGGGCC
CCCGCTCCCGCTGGCCCTCCGAGGGTGAACGACCTCGCTGGGACGTGGGGCAGAGGGC
AGGCGCCAAGAGTGACCCCTGGGACAGCTGGCTGTTTGCAGTTCTGGAGGCAGCCGAGA
TAAAGCGGCTGTTTCCAGTGGGCTCAGGGCCAGAGGGGGCGAGGGGACGCCAGTC
AAGGCCGGCGCTGCTCGGGCTCCCTCTGTGCGGAGGAGGGGGCGGTTGCACAGC
AGCCCCCTGCCCGCCCGCCCGCCGGCGCAGGACCGTGGGACCCGGCTGGTGGCCCT
CCCCCGCCCTGCTCAGGGGCCAGCCCTCTCTGGTCCAGGACCGCCCGCCCGCAGG
CGGCCAGAGAGTCCAGAGTGTAGCCTCCACGCTGTGGGATCTGTATATGCGACAGC
TTAATCAGGCGCAATTTATGGGTCTGGATTGGGTGGGACCGCCCTGCACAGCGG
GGCTGGAAGCCTAAGGCGGTGGGGTGGGGTGAGAGGCCCGCAGACACAGGAGGAGG
CTGGGACACTTCAAGGGTTGACATGCTATGCTGTCAGGATAAATGC

Contig 3 (5347 bp)

AGATGTGTATAAGAGACAGGGGCTGGGTGGGAAGGACAGAGGTGGGGCGGAGGAAATG

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FIGURE 8, CONTD.

GGATGCAGAGCCACCGTGACGCTCTGCTGGCCTTTAGCCTCGCTGAGTCGCAAGAAG
CCCTCGGGCTTGGAAACAGACCCCGGCCCCACCCCAACCCCGGCCCGGATTACCCC
GGCATGGCTGGAGGGCCCGAGAAGCCACCCAGGCTTCCCGTCCGAGCTGGGTGCTGGGC
CCAGCCGAGCGGGCTTGACGCCACGCTTAGCCCTCCCGAGGGAGCCAGGGTCGGAAGGA
AGAGGCCGGCCGGAGGGCCGTGGCCGCTCAGGCTGGAGGGGGCCCGGGTCAGGATGGG
CCCGAGAGCTCCCGCTCCCGGCCATCCGTCACGGAGCTGTACCCAGGAACGTGCTCC
AGACGTGCTTTCTTGGCCGAGGCCCGGAGCAGGCTCCAGGCGCCCAACCCCGAAGC
CCACGCACACCTCGGTCTGCGAACACCTGCCGTCATCCGGTGGCCCGGGTTCGCCGC
GCCCGGCCATCCGGGTGCCCTTCTCCCTGGGTGGGGGCCATGCCCTCAGCGGGCAC
GCAGGCTGTGCAGGTCTGTCTGACTTTCCTCCAAAGACGAGGCCGGCTGCGGGCGCC
CCGACCTCGTCTAGGCCCGTTTGTGCTCACTGGCTGTCTCAGAAAGGGGTGCCACGGG
AAGCCGCTGTTCTTGGCCGCAAGGCAAGGGAGGCCACCCCAAGGTGGCTGAGGGCAAA
TGCCCGAGGGCTCTAAGGAGTCCCTGGGGCCGGCCGGCTGCAGCTTGAGGAGGAGA
CCCTTGGCTGTGCTCCCGGGCAGGTGAGCCACGGCAGGGGGCTCCCGAGAGCTTG
GCAGGAAGCAGTGAGGAAGGGTGAGGATGAAGGCAAGGGGGCTGCGGGGACTTGGGCA
AAGCCCTGAAGAACTGAGTTCTCGGAAAGGCCGGAGCCCTCAGCCGAGCCTCGGCCCT
CGAGGATGGAGGGCCCGCCACCTGCGGCCAGGGTGAGCTGTGATCCGTCGCCCTCG
GGCTCCCGCTGCCCGCCCGGCCACCACTCTCCCTTTTGCTTTGATCACTTGAGT
GCCAGCTTGTGCGGCTGAGCCAGAGACCGCTGCCCGCTGCCCGCAGGCCACGG
GAGCTTCACTTGGCCCTGGCCCTGACTCATCCCTCCCGATGAGGCTTTCTAGCCT
GGCGCGCCCGGGAGCGCCAGCCAGCCCTCGCCCGCTCCCGCAGTGAAGGTGCTGCT
GTGCTGCTTGGGAAGCCCTTGAACAGGGGGCGCAGGTCCACACGGGTGCTCTGGCC
TCCAGCTGCCAGGGAGGGCGGCTCAGGCCAGGGTCCCTCCACGAGAACGCCAGGGC
CTGGGGAACCTGTCTGTGCTAACAGGGCCGCTCCCGGGACTCCAGGAGAGGTGCG
AGGAGCCCTGAGCACCCACCGCACTAAGGGGCCAGCCAGCTCGCGGGTGAGGCAGC
CGCTGGCGCTCATGCTACTGCTCTCTGGCTTTGTGTGTGCGCTGGGTGGGGTG
AGCGAGGTGCCGAAGCGGAAGAGCCACCTCCACTCGGGGACCTATTTCAGCAAGA
AGACGATGGGATGCCGGGATGGACAAGGAACAGGATGAACCTTCTGGAACGACAA
GGCTCCAGGCTGACCGGTCATAGGAAGCGGCTCTAGGCCAATCCACCGTCCACCG
TCCATTCCCGAGCCTCGAGAGGGGGCAGGATGGACCGTGCAGCGTGAGAGAGCTTG
GGCGTCCCGAGGGCAAGTCCAGGGGCACTGACCTCAGAGCCCAACAGGCCACCGGG
GCTGGGCCACAGGGAGCCGGGGCCAGGGTCAGGGTCAGGGCCAGAGTGCGGGAAGG
GTGGCGTGTGCTTGGGGCGGGCGCGCAGCGGCCCTCGCACCCCGCAGAGCCCT
GGAGCTGAGTGAAGCCCGCGGTCACCTTGGCTGGGGTGGGGTCTCTGCGACCGCAC
CCAGCTCAGGTCTCTTGTGTACCGCAGAGGGGGCAGGGTCTGAGCAGGGACAGGG
TGGGGCGCGAGGAAGCCCTTCTCTCTGAGGCTGCCCGGCCCTGGAGCCTCTCTGGG
GCATGCCACCTCTCACAGACGCTCCAGGAGCCCACTTTCTGCTGGCTGGTGAG
GGTGTCTCTACCCGATTCCTGGCCCTGCAGGTGAGTGAGTCCCTGCTAAGCCTGGGG
TTGGAGCAGGTGCAAGGCATCACACACAGCAGCAGAGGCTGTGGGGCCCTGAGAGGC
GCTCCAGGTACCTCTCAGGGGGCTGAGCCCGGGTGGACCCGGGACCTCGCTGCC
CAAAGCCGGCCCTCTCCCGCCCGCCGACAGGGGCCAGAGAAGCAGGTGTGGGGCGG
CACAAACCAAGTCAGCTTCCAGATCTGTCTGGGGCCGCTTGAACCTCGAAGCCCCAG
GCTGGGAGGTGTAGACCCCTGCCAGACGACAGCTGGGGCTGGCTCACAGCTGCCT
GGGGGCCAGGGGTGCACCTGCCCTGTGGGTGGGGTCAGAGGGCAGGGAACCTCGGGA
AGGTCCCGAGGGTCAAGGTGGGGCTAAGCTCCGGTGACCTCTGGGAAGTCTGGGGCTG
GGTTTGTTCAGAGGAGAGAGGGCCAGTAGCCTCAGAGGGGTGTGGCAGGTTGGGAA
GGCCCCAGGTGACCCAGAGCGTGCAGCAAGCCCTTGAAGTGAAGC
GCAAGGGCAGAGGTGGGGTGGGAGCTCGACCCCGAGCCAGGTACACAGGGGGAAG
GGCGAGGGATCCGGCAGGGGCCACACCCGCCACCCAGGCAGCCCAAGCCTTTGGGC
CCGGAGCCAGATGGGCCAGCCAGCTCTGGGAACGCTTCCAGAACTCCCGAGCT
CTGGGTACCAACAGGGCTGCCCGGCCCCAGAGCCCTCGGGCGGGAGACCTTCCCGAGG
GGATCTCTAAGTGGCAAGGCTGTGGGAGGGGTGGTGAGAGGCCACTTGGCGGGA
AGACCCCGAGCCCTGGAGCCCTAGCCACTGCTGCTGGCTCCCTAGGGATCCAGG
GCCATCAGAGAAGCTCAGCGCACTGTTATTTTCAAATGACACTTTTAAAGAAAACA
GCCTCACCAAAATGCTGGCCCTGAGTCTGGAATGTGCAGACAGACAGCTGCCCCCTCCC
AGAGCTGCACGGCCCTCCGGGTGGGGAGGAGCAGGGGGCACCCCTGGGACCGGGCCG
AGGCTGTAGGGCACGGAACGTGTCTTGGGCCCTGTCTCAATTCCCGGTGCCAGTGG
CCCCAATTTCCAGCAGACCCAGAGGGGCCAGCTTGTCTTGGCTGGCCGTGGTCTCT
GTCACCCAGGCTGGAGTTCTGGAAGATTCTGCTCTGCTCCCGTGTGCACATACCACT
CCCCGGGGCAGCCCTGCATCTGTCTGCTGGGCTCCCTGCTGCTCCTGAGGGCT
GCAGCCCGCTGATTTCCAGGTCTCTCCGAGCCCGGCTCCAGGAAGCCCTCCAGG
AGAGCTCAGGAGGGTGGCTCCCTGCGCGCAGCTGTAGACCCCTGGGGCCAGCCCGCG
GCTGTAGGGTCCAGGTTCCTCCACAGCCCTCGGGCAGAGGTGGGGCGCTGGGTCCCTC
GGAGCAACTGGCTCCGAGGCTTGGCTAGACGGGTTCCGGGAGCCCTCCCGAGCGG

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FIGURE 8, CONTD.

CACCCACTGAGTTTTGAACACTTGGCGCCACCCACACCCAGGCGGTGGCCAGGAGGC
CTCCTGGGCAGCAGACAGTCCGTGAGGTGGCCCTGGGGTGGCTCCTGACCTGGGCGCTGG
CCCAGCCCTGGGCACAGCTTTCCAGATCTTGCTGCGCTTCTCCAGGCTGCCTCGGCC
CCTCCCGCTGGGGTGGCCAGCTTTCTGGAGGATGCCACCCCTTGCCATGGTCAGG
GAGGGGCTGAGAAACCCACCTCGTGCTCTGCCCGGCTATGCCAGGGGAACAGGTTTC
CCTCCCGCAGGAGGGGACCGAGTCCCTGACAGCCCACTGCAGAGGGAGGAGGTGCTGG
CTCTGCCCCAGCCCAACCCCGTGGCTTCTGTTCGACGCCCAAGGACTAAA
GGCCGAGGTCTGGAACATCAAGACCCGGGAAGTCCATTGTATTGAATTGAGTGTAAA
TGAGCCTGAGGCTGTGGCTTGCCTTTCCACAATTACCGCTGCCCGGAAGGGCTCCGG
AACCGACACAGCCCCAGGGCCCCCTTGCCCATGTGGGGAGCCAGGCTGGCTGAAGAAG
CCCCATAAGGTGGACCCCACTTTGAGCCCCACAGAGTGGGCCAAGGACAGGTGAGGG
GCTGCCAGGCTCTGGGCTCTCTGCTGCCAGGTGGGCTCCTCGGGGCCAGGCTGG
CCTGCGGAGCTTCCACGCTGAGTTCCCGAGCTGGTATGAGCGTAGTGGACGGCAGCC
ATGCCAGCACTCAGGGGCTGAGGGACAGAGCGGGAATCCAGCCCCGGGTCTCGGC
CCCTAGGATCTCTAGGTGGGGAGCCCAAGGGAGCAGAGGGGTGAACGACAGCTGTGTG
GGGCCCCAGGCTGCCAGCAGACCCCTCTGCTCCACTCTCGGCCGAGTGGGCGCCGAG
ATGCCGGGGCAGTGCCATTTCCAGGGGCCACCGGAGGCTCCAGAGGGAGTGAGGCAGG
AGCTGGGAGGGAGGGCGGGGGCTGGGAGGCAAGAGCGGAGGCCGAGGCGGCTGAG
GAGGCCCGGAGGGGCTGGAGTCAATGACCCAGGGATTATCGTGTGGGTCTTTGAAA
GTTGGCTGAGCAACGCCGGAGCCAGGGTCAAGGAGACGGGACTGGCGGGGCCCGGG
CCCCCTTTCCCTTTCTGGAAGAAAGCTGTTCCAGGTCAAAATCCAGCTCATGATCCG
CCCCCTTTGGGACTGATGTTGAGAGGCCAGTGGTCCAGCACCTCTGTCACCGCCCC
CCACGCTCCCGGGCGGCCAACCCCTGTGGCTGCGAGGTGCGGGCACCTCTCCCTTCG
AAGCAAGCCCTGCCCTGCGTGGGACGCTGATTCTCTCTCTGGGGCTGCACCTTG
ACTGGGGTGGGGGGTGG

Contig 4 (1592 bp)

AGCCCCCAGCCCCCTCCGAGCAGCTGCTGGGCTCAGCGGCTCGCCCCCGATGTGCGGC
CCTCCATAATCAATCATGGAGGGCCGGGCCGGGGGGGGCGGGCCGACCTGTACGCCAGC
TCCAAGGGCAGGGACAGCTGCTGTTCCGGAGGGTTCCAGGGGCCAGCCCCACAGACAG
CGGCCCTCGGCCCCCTTCCCGAGGGGCACCCACGGAGGGCCAGACCGGAGGGACTC
GGGGCCAGAGGCCAGGGCAAGAGTGAAGGCAGCGCCGGTGGGAGCGCGGTGACGGGG
TCCAGGGCTTCAATTCCCAAGGAGCCCATGCCCTGAGCCCGCACTGAGCCCTGTGACGCC
TGTGGGTGCCCGAGGCCGCCACCCCGCCCCCACCAGCTGGGGTCAAGAGAGGGAG
GGGTGGCTGACGGAATGGTAACAGCTGCTCCCCCACCTCGCCGGCTGGACAGGGCTC
GCTTCTCTGCCCCGAGCCCCGGCTGCCCATCCGTACCGCCCCACCCAGGACTGTGCGT
CCAGCCTCCCTCCCTAATCCCCCGCATTTCCGAATTCTCGGGCCACTGTGCTTC
CTCTCAAAATTCCTGGCCCCCTCGCCCCATCCCCGCTATGGGAAAGGGCCGATGCCA
GGACACTTGCTCGTCTCGGCCGGGGGGGGGAGGAGCAGCTGGCTGGGCCCGGACGCTGT
GAGGTGCGGGGGTGGCAGGGAGAAGGGCCAGATTAGGGGGCGTATGGGAAAGCTGGGA
GGGAACGCTACCCAGAGCCCTCCTGCCGAGCCTGTGCTGCTCCTCTCCGCAATTTCTG
GCCTCTGAGTGTCCCTGGAGGGAAGGGACCACTGTGCTCTGCCGGCTCTGGCTCTGCC
AGGAATGTCCATCTGTCCGGGCCGGGTACCTGGCTCAGAGCGTGGGTACAGCTCATCC
AGCCCTGACGCTGCTCTCGGGAACAGTGGATGGGCCAGGCGCCCCCGTACACCCCCGCA
GCTGGGCTCCACAGACGGGCCCGGGATGGCCACGGAGGTGGGGGGCGGCCAGGGCGAG
GCTCCCTCTGGAAGGGCTAGAGTGTGGGCTGCGCGGAGAGGGAGGGCGGACGCCAGGC
CAGGTGCAGCCCCGGGCAGTGTGCTGGGGGCTGTGACCCACGCTGTGACGCTCAAGGGT
CCAGGAGCCCCAGGGACAGAGCCTCAGGGACAGACCTCAGAGCCACAGCAGGAAGCCTG
GTGGCAGTAGCTGGCGGGCCGTGGGGTGTCTCGGCCCTGCAGACAGAGGCAGAGGCAGGC
TCCCTGCTGATGACAGGGGCTTTCTCTGTCCCTGGGGGGCGGAGGGGGCCGACCATGG
ACCCCGGGCTCTCTGCGACGATTCCAGGGCCAGCCTGGTCTCAGGCAGTCCAGGTTG
CACAATGGTCTCCATCGTCCAGAGTTGCAGAGCCAGCACTCTCCACTGGACGGCGGCC
GGGGTGGGCTGACCGGCCCTCAGGGCTCAGGGCCGCGGCCGAGCCNCCGACAGGCC
TTGACCTGTCTTATACACATCTCAACCTG

Contig 5 (831 bp)

TGAGATGTGTATAAGAGACAGGCCTTGACCTGGGCTGGCTCAGCTGCGCGCCCTCTC
CTTGACAGCTCCGCTCGACCCCATCCATCAGCCATTTCTTACCTTCTGTATAAAAA
ACCCGAAGCGCGTGGCCCGTGTCCGTGGGGTGAATCGGCTGCTGTGTGGTGGCTC
CCACCTGGGCGCGGCCCTGAAACACACACCCGGGATGGCTTGCCGGGGCCCTGGT
GGAGGGGGCGGGGGCTCGCTGCTCTGTCTGAAATTTTCGGTCCCATGCCCCGAC
TCCTCTCCGGGCCACCTGCGAGGCCGGCGGTGCCCGGCCACTTTCCGAGGACGG

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FIGURE 8, CONTD.

ACTCAGCATTTCAGGGCACCTGCTGATGGTGCCAGACCCGGGGGCTTCCCGCCGG
GCCGGGCCCCACGTGCCCCCTCAGTGGCCACAGCGGGCTGGGCCAAGGCTGGGAGTTC
TGACAGGGCTGGGGAGGAAGCGGGGAGAGGGGACAGTCTCTGGCGGGGACGAGGG
TGGGGGACAGGTGGGGAGTTCCACAGCCGGGGAGCGGGACGCCGCTTGGCTGCCCT
GGGTCTCAGCGGGGACAGTGCACCAGGAGAGAGCGGCAGACAGTACAGCCACCCG
TTTTATATCTCTCAGGCGGTCTGTGCTTTATGGGGTAAATATGCAGGACATAGAACT
CTGCCACTGGACCCCTTGGCGGGGACACAGCAGCGGCATTGATGCTTCTGGGTGCA
GCCAGCCAGCACACCGGCCAGAGCACCCATCTTCCGATCAACCGGAC

Contig 6 (4634 bp)

CTCTGGGCTAGCACCGTGGGGCTTTGCCAGAGTGGAACTGAACTGGGTCCACCCGGAG
CCAGAGGGCGGTGAATGGGAGGCAGAGCCATCTCGGAATGGACCAGAAGAAAGGGAG
CGGGGGTGGGGGAAGGGGCATCAGATCTGGTCTTCTCTGTGCGCTGCGGTCCCTCTGC
CACCCTCCCCGAAGCTGATCTGGAGCACAGCGCTCGTTAAAGCCGCATCAGAGGCCCA
CTTCTGACAGACGGAAGGGGCGAGTGCCTTCTCACCAGGCTCGCCCTGGGAAGGGCC
CTCCCTGCAGCCAGGAAGCCAGCAGAGGTGACAGAGCCAGGGGCCAGGGCCCCAGGG
ACGGGCTCGCGCGCCGAGCCGGGGTCCCTTGGCGTCCCATCTCTCGTCTGGAGCC
CTCTGGGTGACCACAGGAATGTGAAGCGGCAGCCGGGTGGCGCGGGAGGCGGGTG
GGAGCGGGCGGGGTGGCTCTTACGGCGGGCTGAGAGATGGGCGCCGCTCGGGCC
TGGCGTCTCGTCTCGCGCTCTTACCACTGAGCAAGACACAGAAATGAAGCTCGAA
CGAGCACAGCCAAAGACGGCCGTTCTGTCTTCTTCTTAACTCCCTTGGCTTAGGGT
TTCCCGGCTGGACAGCTGCCCAAGGGCACATGGGCATCCGTCCGGGACATTAGGCA
GTACCAATCCAGGCCACCCAGGCTGTGCCCTGCGTCTGGGCGATTTCAGCCGGGCC
AGAGATGGAGCAGCCACTGCGGGTCCCCGAGTCTCGGTGAGACAGTCAAGGATGGACCT
GGATGGAGACCGGCTGCGGCATGTCCTGGGTGAAGAGGCGTGCAGGCGGTGCTGGG
GGACATGCTGCTGCTCCCTCGGCCAAACATGAAAGCAGCCCTCTCCCCAACCCCA
GCACCAACCCGAGACACCTCGGCGGAGCCAGCACGCCACCGTCAAGTCTCGGT
GTCCAGCTTGGGACAGGTGAGTCCAGATGTCCAGGCTGGAGTGGTCTTGAAGATCC
TAGGGGTCCAGCCAGCACAGGAGGGCCAGGTGAGAGCCCTGTGGTCTTAAGGATGCA
ACCAGGGCGGGCGGGTGCCTGCCCTAGAGGGGTAACCTGGGCCCTGGGGACAGTC
ACCCAGAGGTTCCCAAGAGCCAGCTCGAGGGCCACAGGTGCCAGAGTCCACCTGG
GGAAGGCTGCCCTCTGCCAGCCCCGAGCCGGGCCCTGGCGCCGCGTCCAGCCGG
ACCCCGGGGAGATATTACCCCTGCCCCGTGAATCAGGAGGCCCGAGGCCATGTTT
CAGTCTTTTCTCCATCCAGCCCCCAGGAGAAGAGGTGCTGAAGTGGGTCCCTGG
AGGCTCTGAGCCCCAGAACAGTGCCTCTGAGCAGACGGGCACTCTCAGACAGCTCAC
GCTGGACAAGTCACTCTGCTGCCGCTGATGGGCCCTTGGGAGAAGCAGCATGGTG
AGGAAAGGCCCTGTGCCCTTACCTAATTCACCCAGCCCAAGTCCCACTGGGTGCC
AGCTTCAACCTAAGCAATAATTCGTGCCCTTAAACAAACGCGGGGAATCCACCTGC
CTTCCCCCGCCCCCCCC
ACCCCTGGCTTGACCTCCAAAAGCACTTGAGGGGCTTTCTCCAGACACCTCCAACCC
CGACCCCATGAAGAAGGGGTGATGGGCTGTTACCCCAACAAGCAAGAGAACAAGCCCA
GAGAGGAGTTGGCGTGGACAGCAGGGGTGAGGCCCTTTGCCCGAGGGCAGGGCTGGTG
CCACCTGGGTGAGCGGCAGGCCCTGGAAGAGCACCGGAATGAGCACACTGGGTCTCT
AGAAGGTTCTCCAGACCTCTGGGGCTGAGTCATTCAACACTCTGGGCGGGCAGGG
CTTCTTCTGGGCCCGAGGGACAAGGTCCCTTCTGTCGGGGGTGAGGCCCTGGACCC
CTGTCCCCCGACCCCAACCTCCGCTGGTGAGGGCCGCGCCAGCTCTGGACACAGATC
CCTCAGAGCCCTTCTCCCTCCCTGCTCCTCTTCCCAAGATGCCCGGCTCCAGG
TGGGGCAGCCAGGCGGCAGAAATGTGGTCCAGGCTCTCGGCCCAACCCACACCCCTGC
TGTGCCCTGACAGCTCCAGAGCAGGACAGTGCCTGGTCTGCGTCTGTCTCTCTCA
TGGCACAAACGGTGCCCGCTAGCTTCCCAAGAGAAGGAGATCGTCTCCCGGACG
GACCTGCTCTGCTGTCTCCCGCCGGCTTCAGGGCTCTCCCAAGGGTGGCGCG
AGGAGGCCCTCGCTCCGGCCAGGGGCTCCATCTCCGAGCCGACAGGCTCCGCG
TGTGGTCCGACCTTCTCCCAAGGCCCGGCCATCTCTCGCGTCTCCCAACCCCTG
CCTCTTTCAGCGCCCTTGTCCCAAGGAAGACCTCCACCCGTGCCATTACAGCTC
TCGCCCCACCTCCAGCCACCCCTTCCCATCTCTCTGGAAGCTCCACTTCTTC
CGTCTCCACGGCAGCAGAGGCTCAGAGCTCAGGGTCTTGGGGCTGGAGATGGCC
TGCCCGGGGTCTGCTGACCGCTCTACGGAAGCTGTGCCGGGGGTGGGGGTGCTC
TGCCCAACGGCTGGAGGACGAGCCATCCAGGGCAGCCGGAACCTGCGTCTGGTCT
GAGACGGAGAGGCTGGGTGAGGTGGTGGGGGCTGCACACAGCTTGGCTGGGGTCC
CTAGGTGACAACACTGGCTGAACACTATTGCTGCTCCCTTCCAGGGTGACCTGGGG
TCCCGTGTGGCCCTCAGGGCACAGGGGGCCCAACAGGCTCACAGAACCCAGTGGG
ACTGCACCCAGGGCCACAGAGTGGGGGCACTGGGGTCCAGAAACACCCCAAC

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FIGURE 8, CONTD.

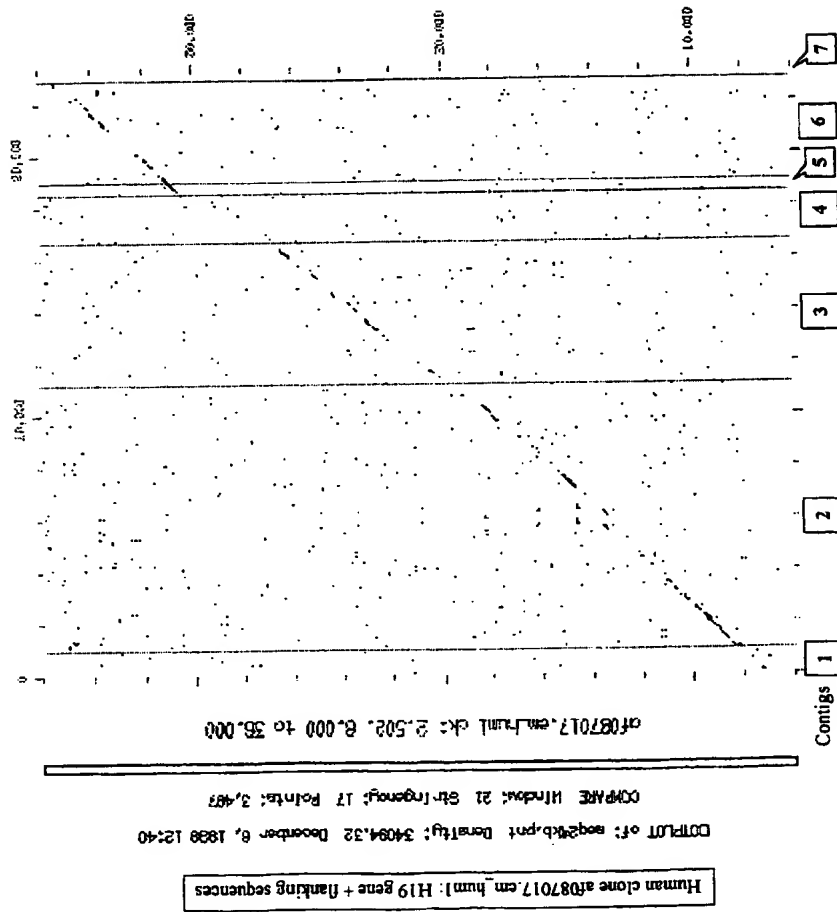
CAGGCCAAGGTGGCCAAGGCCTTACTCGAGCGGGGCTGCCGTCCCAAGAGACTCTGGCC
AGTCGTCCGGATCCAGCTTCCCGGGCCCGGCCCGCTGGGCTCCAGGCGGTCTGGG
GGGCCCTCCCCGGGGTTCGCCCTCCGCTCTCAGCAGCAGGAAGAGGAGCGCGCCAGC
GGATGGGGAGAAGAGGGCGCCCTGGCCATCTTCTCCCCCTGGGACTTGAGGAGGGTCTC
GGCCCGGGCAGGCGGGACCGGGAGCCACAGAGACCCTGGAGGAGGCAGCATGGCGGGAG
GTGACCGGGGAAGAGGGCCGTGTCCAGGGCTCAGAGCCCGGCTGGCCCGCGGCCCTCG
GGAGCGTGGCCGTGACCGCTGGCCGGGAGGTTTGTGCGGTGGGGTTTGAGAAAGT
GCTGAGCTGCTGAGCCACAGGCCAGGCTCAGAGGGGACAGGAAGGAGGTTGCTGCCAG
CCTCGGGCACTGCTGACCATCTCCGTTTCCAGGGCACCAGAGCCACCTAATCTGCCGG
CTCTGTGCCAGGGACAGGCTTGCTGATCTCTCAAGCCGGGCGCTCCGCTTCCCTGG
GAGAGGGTTAAACATCCAGCCCAGCCAGCATCTCGGGCAGGTTCTTGGCTCCCCCGCT
CGTGCTCTCTGAGACCTGTGTCGGCACACCTTCCCTTGAGAGGAGGAGGAGGAGAA
AGCGGATGGAACAGTGACCTGCGAGCCCTGAGGGACCTTCCACGTGCCCGCCCG
CCCCCGCTCTCCGCCCCAGTCTCAGGCCCCAGTCTGATGGAGGGAGGGGACCTC
CGGGCTCCCTGGCTCCCGCCGGCTCCGGAAGACAGGGCCGCTCGGCTGGGGCTGAGGGA
GGGGCCCGAGAGCGAGGAGAGCGAGCCGAGGCAACCCCGCGGCTCTTCAAGAGGAGG
CCTGGCAGGGGAGGGGGTGGCCACCACTGCTGTCTCTCGTCCACAGTGAGGGTGT
GGGTGGGCACTGCCGGGTGGGAAGTGAGAAAGACCCTGGACCCTGGGGCTGGGCCGCC
ACGGGGGAGCGGGTCTGTACGGGACCTGGGGGAGGAGGCGAAGGGCTGGGGCAGAGG
CCGGATCACTTCCAGATTGCTGTGGGACCAAGGGCCGACCTCGGGTGACTTCTTTTG
TGTGCTGGCCACAGGGGGGCCCGCGGAGGTACACGGGAAGGGGCTTCGACCTGGCCT
AACAAAGCCCACTCCGAGGAAGATGCAAGGGGAGGCAGACGGAAGGGCCGAGGGGGGA
TCGGGGGACACCGGGCAGGGCCGGGGCAGAGAAGGGAGGCAGAGGGCAGAGAAGGGAGG
CAGAGGGCAGAGAAGGGAGGCAGAGGGGCCACATGCTTGGAGGGCCAGGGAGGAGCGGGA
ACGGCGTCCGGCTCCAGCGCCGAATCAGGCCCGTCAAGCGGAGGGTGCCTGGACCTGCC
TGGCCTTACGAGCACAGTCAGAGGCTGTCTCTTATACATCTCAACCATCAT

Contig 7 (482 bp)

AGCAATGGGGCCGTGACCTAAGGAGGCAGGCCAGGTGAGTGGGGTGACCTCTCGTGGCC
CCGATGTTTGGAATCCCCAAATCAAAATGACCCATCCGACAAGCTTGCATGCCCTGAGG
TCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGCCCTATAGTGAGTCTGATTAC
AATTCACTGGCCGTCGTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACCT
AATCGCCTTGACGACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACC
GATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTT
CTCCTTACGCATCTGTGCGGTATTTACACCGCATATGGTGCACTCTCAGTACAATCTGC
TCTGATGCCGATAGTTAAGCCAGCCCCGACACCCGCCAACCCGCTGACGCGAACCC
TT

FIGURE 9

Human clone af087017.em_hum1: H19 gene + flanking sequences



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FIGURE 10

IDENTIFIED POLYMORPHISMS:POLYMORPHISMS TYROSINE HYDROXYLASE GENE - CONTIG C3 (figure 6)

| | | |
|---|-----------------------------|---------|
| 1 | GGATCCAGCC (A:T) GCAGCC | 1081 bp |
| 2 | ACAACCCCC (-:C) TCCCACAG | 1149 bp |
| 3 | TGCGGAGGGG (A:G) GACCTG | 1186 bp |
| 4 | AGGT (CAAGGCCAGGT: -) CGAGG | 1210 bp |

POLYMORPHISMS INSULIN-IGF2 - CONTIG C4 (figure 6)

| | | |
|----|-----------------------------|---------|
| 5 | CCC (C:A) CCCC (A:C) CGCCGC | 438 bp |
| 6 | CCC (C:A) CCCC (A:C) CGCCGC | 443 bp |
| 7 | CGCCGCAGCA (G:A) GCCG | 455 bp |
| 8 | GCTTATGG (G:A) GCCGGG | 503 bp |
| 9 | CACGGC (T:C) TC (G:A) GAGCA | 525 bp |
| 10 | CACGGC (T:C) TC (G:A) GAGCA | 528 bp |
| 11 | GTCTGC (A:G) GGCAGGTG | 571 bp |
| 12 | CAAGCCCGG (G:T) CGGTT | 636 bp |
| 13 | ACCTC (A:G) AGGCCCCCA | 710 bp |
| 14 | GC (C:T) GGGCCCAGCCGC | 867 bp |
| 15 | ACCAGCTG (C:T) GTTCCC | 903 bp |
| 16 | GGC (C:G) CTCTGGGCGCC | 1148 bp |
| 17 | GGGGG (C:T) GTCCCGGGA | 1305 bp |

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FIGURE 10, CONTD.

| | | |
|----|-----------------------|---------|
| 18 | GCGGT (C:T) GGGGGAGTT | 1320 bp |
| 19 | CGCCC (C:T) GTCCCGCT | 1400 bp |
| 20 | TCCC (G:A) TCTGCCGGCC | 1519 bp |
| 21 | GA (T:A) GCCCCATCCCCC | 1547 bp |
| 22 | GG (C:T) GGCTGCTGCGGC | 1607 bp |
| 23 | TGGCTGC (G:A) GTCTGGG | 2222 bp |

POLYMORPHISMS IN CODING REGION - CONTIG C10 (figure 6)

| | | |
|----|---------------------------|---------|
| 24 | GCGCA (G:T) TGATTGGCA | 341 bp |
| 25 | CGCCCCCCCC (-:C) (G:C) GG | 2247 bp |
| 26 | CGCCCCCCCC (-:C) (G:C) GG | 2248 bp |
| 27 | GCAGCCGGCTC (C:T) TGG | 2257 bp |
| 28 | GTTGTG (C:T) TCTGGGA | 2413 bp |

MICROSATELLITES

| | | |
|----|---|---------------------------|
| 29 | PIGQTL1: (AT) ¹¹ | 112 to 133 bp Contig 57 |
| 30 | PIGQTL2: (GT) ⁸ GCACCGTGTGGGTGTGTAC (GT) ¹⁷ | 1074 to 1144 bp Contig 95 |
| 31 | PIGQTL3: (CA) ¹⁹ | 223 to 260 bp Contig 105 |

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